

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: August 27, 2003, 08:06:46 ; Search time 4141 Seconds
(without alignments)
2943.991 Million cell updates/sec

Title: US-09-811-094-33
Perfect score: 1543
Sequence: 1 MTEQAISPAKPLAGIAAA.....LRGMCAPVLYLDELKRYI 298

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters: -DEV-xlp
-MODE-frame+pn.model -DEV-xlp
-O/-cgcn2.1/USPTO.spool.p/US09811094/runat.26082003.110450.8020/app.query.fasta.1.455
-DB-Genembl -OEMT-fastp -SUPFIX-p2n.rge -MINMATCH-0.1 -LOOEXT-0 -LOOEXT-0
-UNITS-bits -START-1 -END-1 -MATRIX-biosum62 -TRANS-human40.coi -LIST-45
-DOCCALIGN-200 -THR.SCORE-pot -THR.MAX-100 -ALIGN-15 -MODE-LOCAL
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-USER-US09811094.cgcn.1.1.4958-erunat.26082003.110450.8020 -NCPV-6 -ICPD-3
-NO_MMAP -LARGEUDERY -NEG.SCOSES-0 -WAIT -DSPBLOCK-100 -LONGLOG
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-FGAPEXT-7 -YGAPOP-10 -YGAEXT-0.5 -DELOP-6 -DELEXT-7

Database : GenEmbl.*
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41: em.htgo.other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1543	100.0	897	6 AX134720	AX134720 Sequence
2	1543	100.0	897	6 AX301848	AX301848 Sequence
3	1543	100.0	1193	9 BC008935	BC008935 Homo sapi
4	1543	100.0	1308	9 BC007295	BC007295 Homo sapi
5	1543	100.0	1344	9 AY007135	AY007135 Homo sapi
6	1543	100.0	1366	9 BC007850	BC007850 Homo sapi
7	1543	100.0	1399	9 BC031912	BC031912 Homo sapi
8	1543	100.0	1466	9 BC008737	BC008737 Homo sapi
9	1537	99.6	1455	9 BC014775	BC014775 Homo sapi
10	1512	98.5	1349	4 BOVT27RANS	M24103 Bovine ADP/
11	1474	95.5	1010	5 AB088686	AB088686 Gallus ga
12	1454	94.2	897	6 AX134719	AX134719 Sequence
13	1454	94.2	897	6 AX301847	AX301847 Sequence
14	1454	94.2	1228	9 HUMATPC	J02683 Human ADP/A
15	1451	94.0	1146	4 AB065433	AB065433 Bos tauru
16	1451	94.0	1215	10 RATYANR2	D12771 Rattus norv
17	1446	93.7	1266	5 AF506216	AF506216 Danio rer
18	1445	93.6	897	10 MMT10A04	U10404 Mus musculu
19	1445	93.6	1236	10 BC004570	BC004570 Mus muscu
20	1445	93.6	1244	10 BC0027316	BC0027316 Mus muscu
21	1445	93.6	1280	10 MMANTAP	U27316 Mus musculu
22	1424	92.3	1196	6 AX401651	X70847 M. musculus
23	1424	92.3	1196	10 RATYANR1	AX401651 Sequence
24	1422	92.2	932	4 AB009386	D12770 Rattus norv
25	1422	92.2	1194	4 BOVT1RANS	AB009386 Oryctolag
26	1421	92.1	1289	5 AF231347	M24102 Bovine ADP/
27	1421	92.1	1316	5 BC043821	AF231347 Xenopus l
28	1418	91.9	1070	10 BC026925	BC026925 Mus muscu
29	1418	91.9	1142	10 BC003791	BC003791 Mus muscu
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31	1412	91.5	1273	10 MM27315	U27315 Mus musculu
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35	1409	91.3	1318	5 AB008461	AB008461 Rana rugo
36	1409	91.3	1319	9 BC008664	BC008664 Homo sapi
37	1406	91.1	1313	5 AB008458	AB008458 Rana rugo
38	1406	91.1	1318	5 AB008459	AB008459 Rana rugo
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40	1402	90.9	1310	5 AB008457	AB008457 Rana rugo
41	1394	90.3	231319	10 AC122916	AC122916 Mus muscu
42	1385.5	89.8	894	6 AX134718	AX134718 Sequence
43	1385.5	89.8	894	6 AX301846	AX301846 Sequence
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ALIGNMENTS

RESULT 1

AX134720 897 bp DNA linear PAT 29-MAY-2001
 LOCUS AX134720
 DEFINITION Sequence 3 from Patent WO0132876.
 ACCESSION AX134720
 VERSION AX134720.1 GI:14271237
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1 Murphy A.N., Clevenger W., Wiley S.E., Andreyev A.Y., Frigeri L.G.,
 Velicogri G. and Davis R.E. 1999. Methods for determining interactions of
 mitochondrial components, and for identifying agents that alter
 such interactions.
 JOURNAL Patent: WO 0132876-A 3 10-MAY-2001;
 MITOKOR (US)

FEATURES
 source Location/Qualifiers
 1..897
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

BASE COUNT 174 a 274 c 287 g 162 t
 ORIGIN

Alignment Scores:
 Pred. No.: 8.86e-145 Length: 897
 Score: 1543.00 Matches: 298
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 0

US-09-811-094-33 (1-298) x AX134720 (1-897)

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 DB 1 ATGACGGAAGAGGCGCATCTCTCGCAAGATCTTGGCGGAGCATCGCGCGCGC 60
 OY 21 IleSerLysThrAlaValAlaProIleGluArgValIleLeuLeuGlnValGlnHis 40
 61 ATCTCCAAAGAGGCGCGTCCGATCGAGCGGATCAAGCTCTCTCGAGTCCAGCAGC 120
 DB 61 ATCTCCAAAGAGGCGCGTCCGATCGAGCGGATCAAGCTCTCTCGAGTCCAGCAGC 120
 OY 41 AlasSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
 121 GCCAGACAGCATGCGCGCGGAGCAAGCATCAAGGCGATCGTGCATGTCTCCG 180
 DB 121 GCCAGACAGCATGCGCGCGGAGCAAGCATCAAGGCGATCGTGCATGTCTCCG 180
 OY 61 IleProLysGluGlnGlyValIleuSerPheTyrArgGlyAsnLeuAlaAsnValIleArg 80
 181 ATCCCAAGAGAGGCGCGTCTCTCTGAGGAGGCGCAAGCTTGCAGCATTCATTCGC 240
 DB 181 ATCCCAAGAGAGGCGCGTCTCTCTGAGGAGGCGCAAGCTTGCAGCATTCATTCGC 240
 OY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysGlnTyrLysGlnIlePheLeu 100
 241 TACTTCCCACTCAAGCCCTCACTGCGCTTCAAGGATACGATCAAGCATCTTCTCG 300
 DB 241 TACTTCCCACTCAAGCCCTCACTGCGCTTCAAGGATACGATCAAGCATCTTCTCG 300
 OY 101 GlyIleValAspLysHisThrGlnPheTyrArgGlyPheAlaGlyAsnLeuAlaSerGly 120
 301 GGGGCGCTGAGCAAGACACGAGATTCGAGAGGAGTTCGGGCAAGCTGCGCTCCGCGC 360
 DB 301 GGGGCGCTGAGCAAGACACGAGATTCGAGAGGAGTTCGGGCAAGCTGCGCTCCGCGC 360
 OY 121 GlyAlaIleAlaGlyAlaThrSerLeuGlyPheValTyrProLeuAspPheAlaThrArg 140
 361 GGTGCGGCGCGCGCGCTCTCTGCTGCTGATCCCGCTGATTTGCGCAAGACCGCGC 420
 DB 361 GGTGCGGCGCGCGCGCTCTCTGCTGCTGATCCCGCTGATTTGCGCAAGACCGCGC 420
 OY 141 LeuAlaIleAspValAlaLysSerGlyThrGlnArgGlnPheArgGlyLeuGlyAspCys 160
 421 CTGGCAGCGAGCTGGGAAAGTCAGGACAGAGCGGAGTTCGAGCGCTGGGAGACGCGC 480
 DB 421 CTGGCAGCGAGCTGGGAAAGTCAGGACAGAGCGGAGTTCGAGCGCTGGGAGACGCGC 480
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 481 CTGGTGAAGATCAACCAAGTCGAGGCGATCCGGGCGCTGACCAAGGCGCTTCAGTCTCC 540
 DB 481 CTGGTGAAGATCAACCAAGTCGAGGCGATCCGGGCGCTGACCAAGGCGCTTCAGTCTCC 540
 OY 181 ValGlnGlyIleIleIleTyrArgAlaIleAlaTyrPheGlyValTyrAspThrAlaLysGly 200

DB 541 GTTCAGGAGATCATCATCTACCGCGCGCGCTACTTCCGCTGATGATGATGCGCAAGGCGC 600
 OY 201 MetLeuProAspProLysAsnThrHisIleValIleSerPheMetIleAlaGlnThrVal 220
 DB 601 ATCTCTCCCGAGCCCAAGACACGACATCGTGTGAGCTGATGATGCGGAGACCGCGC 660
 OY 221 ThrAlaValAlaGlyValAlaSerTyrProPheAspThrValArgArgMetMetMet 240
 DB 661 ACGGCGGTGGCGCGGTGTGTCTTACCTTTCGACGAGTGGCGGCGCGGATGATGATG 720
 OY 241 GlnSerGlyArgLysGlyValAlaAspIleMetTyrThrGlyThrValAspCysTyrArgLys 260
 DB 721 CAGTCCGCGCGCAAGAGAGCTGATCATATATACAGCGGACCGCTGATGATGATGATG 780
 OY 261 IlePheArgAspGluGlyLysAlaPhePheLysGlyAlaTyrSerAsnValIleArg 280
 DB 781 ATCTTCAGAGATGAGGCGGAGCAAGCGCTTCTTCAAGGAGTGTGTGTCCAGCTCTCCG 840
 OY 281 GlyMetGlyGlyAlaPheValIleuValIleuTyrAspGluLeuLysValIle 298
 DB 841 GGCATGGGCGCGCGCTCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATG 894

RESULT 2
 AX301848 897 bp DNA linear PAT 30-NOV-2001
 LOCUS AX301848
 DEFINITION Sequence 3 from Patent WO0185944.
 ACCESSION AX301848
 VERSION AX301848.1 GI:17382905
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1 Anderson C.M., Davis R.E., Clevenger W., Wiley S.E., Miller S.W.,
 Szabo T.R., Ghosh S.S., Moos W.H., Pel Y. and Carroll A.K. 1999.
 Production of adenine nucleotide translocator (ant), novel ant
 ligands and screening assays therefor
 Patent: WO 0185944-A 3 15-NOV-2001;
 MITOKOR (US)

FEATURES
 source Location/Qualifiers
 1..897
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

BASE COUNT 174 a 274 c 287 g 162 t
 ORIGIN

Alignment Scores:
 Pred. No.: 8.86e-145 Length: 897
 Score: 1543.00 Matches: 298
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 0

US-09-811-094-33 (1-298) x AX301848 (1-897)

OY 1 MetThGUGInAlaIleSerPheAlaIAspPheLeuAlaGlyGlyIleAlaAla 20
 1 ATGACGGAAGAGGCGCATCTCTCGCAAGATCTTGGCGGAGCATCGCGCGCGC 60
 DB 1 ATGACGGAAGAGGCGCATCTCTCGCAAGATCTTGGCGGAGCATCGCGCGCGC 60
 OY 21 IleSerLysThrAlaValAlaProIleGluArgValIleLeuLeuGlnValGlnHis 40
 61 ATCTCCAAAGAGGCGCGTCCGATCGAGCGGATCAAGCTCTCTCGAGTCCAGCAGC 120
 DB 61 ATCTCCAAAGAGGCGCGTCCGATCGAGCGGATCAAGCTCTCTCGAGTCCAGCAGC 120
 OY 41 AlasSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
 121 GCCAGACAGCATGCGCGCGGAGCAAGCATCAAGGCGATCGTGCATGTCTCCG 180
 DB 121 GCCAGACAGCATGCGCGCGGAGCAAGCATCAAGGCGATCGTGCATGTCTCCG 180
 OY 61 IleProLysGluGlnGlyValIleuSerPheTyrArgGlyPheAlaGlyAsnLeuAlaSerGly 80
 181 ATCCCAAGAGAGGCGCGTCTCTCTGAGGAGGCGCAAGCTTGCAGCATTCATTCGC 240

Db	181	ATCCCAAGGACGAGGGCGTGTCTCTCTTGAGGGGGCAACCTTGGCAACGTATTCGC	240
Qy	81	TyrPheProthrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu	100
Db	241	TACTTCCCTCCACTCAAGCCCTCAACTTGGCTTCAAGATTAAGTACAAAGATCTTCTCG	300
Qy	101	GlyValLysAlaPheLysHisThrGlnPheThrArgTyrPheAlaGlyAsnLeuAlaSerGly	120
Db	301	GGGGGCGCTGGCAAGCACACGCACTTCCTGGAGGTACTTGGGGCAACTGGCCCTCCGCG	360
Qy	121	GlyAlaAlaGlyAlaThrSerLeuSerLysPheValLyrProLeuAsnPheAlaArgThrArg	140
Db	361	GGTCCGGGCGGGGGAGACTCTCCTTGTCTGTCTGTAACCCGCTGGATTTTCCAGAACCCGC	420
Qy	141	LeuAlaAlaAspValGlyLysSerGlyThrGlnArgGlnPheArgGlyLeuGlyAspCys	160
Db	421	CTGGCACCGGACGCGTGGAAAGTCAGGACAGAGCGCGAGTTCGAGGCGCTGGAGACTGC	480
Qy	161	LeuValLysIleThrLysSerAspGlyTyleArgGlyLeuTyrGlnGlyPheSerValSer	180
Db	481	CTGGTGAAAGATCAACCAAGCTCGACGGGATCGGGGGCTGTACCAAGGGCTTCAGTCTCC	540
Qy	181	ValGlnGlyIleIleIleTyrArgAlaAlaThrPheGlyValLyrAspThrAlaLysGly	200
Db	541	GTCGAGGGGCACTATCATCTACCGGGCGGCTTCTGGCTGTACATGATCGGCAAGGGC	600
Qy	201	MetLeuProAspProLysAsnThrHisIleValValSerTyrMetIleAlaGlnThrVal	220
Db	601	ATGCTCCCGGACCCCAAGAACACGACACATGTTGGTAGCTGAGTATGCGGACAGCGTG	660
Qy	221	ThrAlaValAlaGlyValValSerTyrProPheAspThrValAlaGlnArgMetMet	240
Db	661	ACGGCCGTGGCGGGCGGTGTCTTACCCCTTCACACAGGGCGGGCGGCGATGTGATG	720
Qy	241	GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysThrArgLys	260
Db	721	CAGTCCGGGCGCCCAAGAGACTGATCATCTGTACACGGGACCGTGCATGTGTGGAGAG	780
Qy	261	IlePheArgAspGlnGlyGlyLysAlaPhePheLysGlyAlaTyrPheAsnValLeuArg	280
Db	781	ATCTTCAGAGATGAGGGGGCGGACGCTTCTTCAAGGGTGGGTGTCACAGCTCTCGGG	840
Qy	281	GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysValIle	298
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RESULT 3			
LOCUS	BC008935	1193 bp	mRNA
DEFINITION			linear PRI 12-JUL-2001
LOCUS			
DEFINITION			Homo sapiens, similar to solute carrier family 25 (mitochondrial
LOCUS			carrier; adenine nucleotide translocator), member 5, clone MGC:2387
DEFINITION			IMAGE:2824067, mRNA, complete cds.
ACCESSION			BC008935
VERSION			BC008935.1 GI:14286273
KEYWORDS			MGC.
SOURCE			Homo sapiens (human)
ORGANISM			Homo sapiens
			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
			Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE			1 (bases 1 to 1193)
AUTHORS			Strausberg,R.
TITLE			Direct Submission
JOURNAL			Submitted (29-MAY-2001) National Institutes of Health, Mammalian
			Gene Collection (MGC), Cancer Genomics Office, National Cancer
			Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
			USA
REMARK			NIH-MGC Project URL: http://mgc.ncl.nih.gov
COMMENT			Contact: MGC help desk
			Email: cgapbs-r@mail.nih.gov
			Tissue Procurement: DCM/DMP
			CDNA Library Preparation: Rubin Laboratory
			CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNLT)
			DNA Sequencing by: Institute for Systems Biology

<http://www.systemsbio.org>
contact: amadan@systemsbio.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Kellerman and Anuradha Madan

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILNl at: <http://image.llnl.gov>
Series: IRAL Plate: 2 Row: n Column: 21
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 9956038.

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 LVKTKTSKDGIRGLYQGVSRFSVQGIITIRAVFEGVYDPAKGLDLPKRNTHIVSMINQ
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Alignment Scores:	
Pred. No.:	1.27e-144
Score:	1543.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	9
Length:	1193
Matches:	298
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-811-094-33 (1-298) x BC008935 (1-1193)

OY	1	MethrhtglutinalaIleSerPheuaIalysaSPheueuaIagIyglIleIaIaIa	20
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OY	21	IleSerIySPrralIaValaIaProIleIuIryValIySLeuIeueGInValGIhIIs	40
Dd	154	ATCTCCAGACGGCCGCGTGGCTCCGATCGACGGGGGTCAAGCTGCTGTCAGAGTCAGAC	213
OY	41	AlaSerIySGInIlealIaIaAspIySGInIryIySGIleValaSPCyIleValaIrg	60
Dd	214	GCCAGCAAGCAGATCGCGCCGACAGACAGTACAAAGGCCATCGTGAATGTGTCCG	273
OY	61	IleIrrPolySGIuGIuGIyValIeuserPheIrrPaIrgIyAsnIeuaIaasValIleIarg	80
Dd	274	ATCCCAAGGAGCGAGGGCTGCTCTCTTCCTTCGGAGGGGCAACCTTGCCACAGTATTCGC	333
OY	81	TyrPhePrrOrrhIaIaIeuaSPheIaPheIySaSPyIryIySGInIlePheIeu	100
Dd	334	TACTTCCCCACTCAAGCCCTCAACTCTGCCCTCAAGGATTAAGTCAACAGACATCTCTCG	393
OY	101	GlySGIyValaSPyIySHIsthrGInPheIrrPaIrgIyPheuaIagIyAsnIeuaIaSerGIy	120
Dd	394	GGGGGCGTGCACAGCACACGCACTTCGGAGGTACTTTGGGGCAACCTGCGCTCGGC	453
OY	121	GlyIaIaIaGIyIaIaIaIrrSerIeueCysPheValIyrrProIeuaSPheuaIaIaIrrIaIrg	140
Dd	454	GGTGGCGGGCGGACCTCCCTGTGCTCTGTACCGCGCTGAGTATTTGGCCAGAACCGC	513

[illegible]

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/BLM at: <http://image.llnl.gov>

Series: IRM1 Plate: 20 Row: 1 Column: 14

This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

Location/Qualifiers

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- /mol_type="mRNA"
- /db_xref="taxon:9606"
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- /tissue="Brain, neuroblastoma"
- /clone_lib="NIR_MGC_19"
- /lab_host="DH10B-R"
- /note="Vector: pOTB7"
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- /codon_start=1
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- /protein_id="AAH07850.1"
- /db_xref="GI:14043791"
- /translation="MTBOAISFAKDFLAGGIANIAISKTVANPIERYKLLLOVHASKR
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BASE COUNT	287 a	419 c	409 g	251 t
ORIGIN				
Alignment Scores:				
Pred. NO.:	1.5e-144	Length: 1366		
Score:	1543.008	Matches: 298		
Percent Similarity:	100.008	Conservative: 2		
Best Local Similarity:	100.008	Mismatch: 0		
Query Match:	100.008	Indels: 0		
DB:	9	Gaps: 0		

US-09-811-094-33 (1-298) x BC007850 (1-1366)

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QY	21	Ilaserlystfualaialaialaprolielguarvallylsleuleuleuglnaiglnhis	40
Db	161	ATCTCCAGAGCGCCGCTGGCTCGATCGAGCGGGGTCAAGCTGCTGTGAGAGTCCACAC	220
QY	41	Alaserlysglnllealaialaasplysglntrylysglyllevalaspysllevalarg	60
Db	221	GCCAGAGACAGATCGCCGCCGACAGCGATCAAGGGCATCTGGACATCTTGTCGC	280
QY	61	Illeprolysgluinglnlyalleaserpheetrparglyasnlleualasnlvalilearg	80
Db	281	ATCCCAAGAGACAGGGCGTGTGCTCTTCGAGAGGGCAACCTGCCAACGTCAATGCC	340
QY	81	Tyrpheetrthglnaialaaleuanphealaphelysasptrytyrlysglnllepheu	100
Db	341	TACTCTCCACATCAAGCCCTCACTTCGCTTCCAAGGATTAAGTACAAGCAGATCTTCCTG	400
QY	101	Glyglyvalaspysahstthglnpheetrparglyrrephaelaglyasnlleualasergly	120
Db	401	GGGGGGGTGACACACACACAGATCTTGAGAGTACTTTGGGGCAACCTGGCCCTCGGC	460
QY	121	Glyalaalaglyalathrserleucysphevaltyrproleuasaphealargtharg	140
Db	461	GGTGGCGGGCGGCGCACCTCCCTGCTTCGTGCTGTCGCCCGGATTTGGCAAAACCGC	520
QY	141	Leualalaaspvalaglylyserglythrngluarglnpheargglyleuglaspys	160

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Db      521 CTGGCAGCGGAGCTGGGAAAGTACAGCAGACGCGAGTTCGAGCGCTGGGAGACTGC 580
Qy      161 LeuValIysIleThrIysSerAspGlyIleArgGlyLeuTyrgInglyPheSerValSer 180
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Qy      181 ValGInglyIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 200
Db      641 GTGCAGGCGATCATCTACACGCGGCGCTACTTGGCGCTGTACATACGAGCCCAAGGGC 700
Qy      201 MetLeuProAspProIysAsnThrHisIleValIleSerIlePheIleIleIleIleIleIle 220
Db      701 ATGCTCCCGACACCCACAGAACGACGATGCTGTGATGATGATGATGATGATGATGATGATG 760
Qy      221 ThrAlaValAlaGlyValIleSerIleIleIleIleIleIleIleIleIleIleIleIleIle 240
Db      761 ACGGCGGTGGCGCGCGGTGCTTACCCCTTGACACGCGTGGCGGCGGCATGATGATGATG 820
Qy      241 GlnSerGlyArgGlySerGlyAlaAspIleMetIleIleIleIleIleIleIleIleIleIle 260
Db      821 CAGTCCGGGCGGCAAGAGAGCTGACATCATGTACACGCGGCGACCGCTGCTGGAGAGAG 880
Qy      261 IlePheArgAspGlnGlyIleGlyIleIleIleIleIleIleIleIleIleIleIleIleIle 280
Db      881 ATCTTCAGAGATAGAGGGGCGGACAGGCTTCTTCAAGGGTCCGTGATCCAAAGCTCTGG 940
Qy      281 GlyMetGlyIleValIlePheValIleValIleIleIleIleIleIleIleIleIleIleIle 298
Db      941 GCGATGGGGGGCGGCGCTTGGTGTGCTGTACGAGAGCTCAAGAAAGTGATC 994

RESULT 7
BC031912      1399 bp      mRNA      linear      PRI 26-JUN-2002
LOCUS      Homo sapiens, solute carrier family 25 (mitochondrial carrier);
DEFINITION      adenine nucleotide translocator, member 6, clone MGC:29984
VERSION      BC031912.1 GI:21594692
KEYWORDS      MGC.
SOURCE      Homo sapiens (human)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS      Strausberg, R.
TITLE      Direct Submission
JOURNAL      Submitted (06-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK      NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT      Contact: MGC help desk
Email: gcrabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Guanatone, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNLN at: http://image.lnl.gov
Series: IRAC Plate: 42 Row: P Column: 5
This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
identity to protein.

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location/Qualifiers

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TVYAVGVVSYPEDTVRRMMQSGRGRADIMYTGTVDCWKIFRDEGGKAFKFGAMS
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BASE COUNT      300 a      419 c      414 g      266 t
ORIGIN
Alignment Scores:
Pred. No.:      1,55e-144      Length:      1399
Score:      1543.00      Matches:      298
Percent Similarity:      100.00%      Conservative:      0
Best local Similarity:      100.00%      Mismatches:      0
Query Match:      100.00%      Indels:      0
DB:      9      Gaps:      0

US-09-811-094-33 (1-298) x BC031912 (1-1399)
Qy      1 MetThrGlnIleAlaIleSerPheAlaIleValAspPheLeuAlaGlyIleIleAlaAla 20
Db      38 ATGACGAAACAGGCGATCTCTTCGCAAGAACTCTTGGCGGAGGACATCGCGCGCC 97
Qy      21 IleSerIleThrAlaValAlaProIleGluArgValIleLeuLeuGlnIleAlaGlnHis 40
Db      98 ATCTCCAAAGAGCGCGCGTGGCTCCGATGACGGGTCAAGCTGCTGCTCGACGCTCAGAC 157
Qy      41 AlasSerIleGlnIleAlaAlaAspIleGlnIleIleValIleValAspCysIleValArg 60
Db      158 GCCAGCAAGAGATCGCGCGCGCAAGCAAGCAAGGCGCAGCTGCATGATGTCGC 217
Qy      61 IleProIleGlnIleGlnIleValIleSerPheIleIleValIleValIleValIleVal 80
Db      218 ATCCCAAGAGAGCGGCGGTGCTCTCTGTGGAGGGGCAACCTTGCCAACTGATTCGC 277
Qy      81 TyrPheProThrGlnAlaIleAsnPheAlaPheIleAspIleIleValIleValIleVal 100
Db      278 TACTTCCCACTCAAGCCCTCACTTCCCTTCAAGATTAAGTCAAGCAAGATCTTCTCG 337
Qy      101 GlyGlyValAspIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 120
Db      338 GGGGCGCTGTGACAAAGCAGCAGCAAGCTTGTGAGGACTTGTGCGGCAACTGCGCTCGGC 397
Qy      121 GlyAlaIleAlaGlyAlaIleIleIleIleIleIleIleIleIleIleIleIleIleIle 140
Db      398 GGTGCGCGCGCGGCGGACCTCTCTGTGTGTGATACCGCGTGGGCAAGAACCGCG 457
Qy      141 LeuAlaIleAspValAlaGlyIleSerGlyIleIleIleIleIleIleIleIleIleIleIle 160
Db      458 CTGGCAGCGGACGCGGAAAGTCAAGCAGCAGAGCGGCAAGTTCAGAGCTCGGAGACTGC 517
Qy      161 LeuValIleIleThrIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 180
Db      518 CTGCTGAAGATCACCAAGTCCGACGCGATCCGGGCGCTGTACACGAGGCTTCAAGTCTCC 577
Qy      181 ValGInglyIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 200
Db      578 GTGCAGGCGATCATCTACCGGCGGCTACTTGGCGCTGTACATACGAGCCCAAGGGC 637

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OY 201 MetLeuProaspProlysaAsnThrHisIleValSerTyrMetIleAlaGlnThrVal 220
DB 638 ATGCTCCCGACCCAGACACGACATCGTGACCTGGATGATGCGGAGACCGG 697
OY 221 ThrAlaValAlaGlyValAlaSerTyrProPheAspThrValArgArgMetMet 240
DB 698 AGGGCGGCGGCGGCGTGCTCTCTACCCCTTCGACAGCGCGCGCGCATGATGATG 757
OY 241 GlnSerGlyArgGlyGlyValAlaAspIleMetTyrThrGlyThrValAlaAspCysTrpArg 260
DB 758 CAGTCGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 817
OY 261 ThrPheArgAspGluGlyGlyValAlaPhePheGlyValAlaTrpSerAsnValLeuArg 280
DB 818 ATCTTCAGATGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 877
OY 281 GlyMetGlyGlyAlaPheValIleuValIleuValIleuValIleuValIleuValIleu 298
DB 878 GGCATGGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 931

RESULT 8 1466 bp mRNA linear PRI 12-JUL-2001
BC008737 Homo sapiens, similar to soluble carrier family 25 (mitochondrial)
LOCUS carrier; adenine nucleotide translocator), member 5, clone MGC:3042
DEFINITION IMAGE:3342722, mRNA, complete cds.

ACCESSION BC008737.1 GI:14250566
VERSION MGC.
KEYWORDS Homo sapiens (human)
SOURCE Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
ORGANISM 1 (bases 1 to 1466)
Strausberg, R.
Direct Submission
Submitted (25-MAY-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 1A03, Bethesda, MD 20892-2590,
USA

REMARK NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
Contact: MGC help desk
Email: gcaps-help@mail.nih.gov

COMMENT Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@nigr.nih.gov
Shevchenko, Y., Welther, R.D., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
Dieterich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Leisner, R.,
Lim, M., Maduro, O.L., Mastaglio, C., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Snyder, B., Stentilopoulos, S., Thomas, P.J.,
Tsong, E.E., Touchman, J.W., Tsougenou, C., Vogel, J.L., Walker, M.A.,
Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/TLNU at: <http://image.tlnu.gov>
Series: IRL Plate: 5 Row: O Column: 23
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency OK
analysis.

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NVRMGSAFVLVDLTKVTL 273 t

BASE COUNT 327 a 441 c 425 g 273 t
ORIGIN
Alignment Scores:
Pred. No.: 1.64e-144 Length: 1466
Score: 1543.00 Matches: 298
Percent Similarity: 100.00% Conserved: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-811-094-33 (1-298) x BC008737 (1-1466)

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OY 21 IleSerTyrThrAlaValAlaPheIleGluArgValIleuLeuGlnValGlnHis 40
DB 149 ATCTTCAGATGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 208
OY 41 AlaSerGlyGlnIleAlaIleAspIleGlyIleValAlaAspCysIleValArg 60
DB 209 GCGACAGACAGATCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 268
OY 61 ThrProlyGluGlnGlyValIleuSerPheTyrPargIleValIleuAlaAsnValIleArg 80
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OY 121 GlyAlaIleAlaGlyAlaThrSerIleCysPheValIleuValIleuAlaIleuArg 140
DB 449 GGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 508
OY 141 LeuAlaIleAspValIleGlySerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
DB 509 CTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 568
OY 161 LeuValIleIleThrIleSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
DB 569 CTGTGAATATCAACAACTCGGAGCGGATCGGGGCGGCTGTACAGGCGGCTTCAAGTCTCC 628
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DB 629 GTGAGGCGATCATCTACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 688
OY 201 MetLeuProaspProlysaAsnThrHisIleValSerTyrMetIleAlaGlnThrVal 220
DB 689 ATGCTCCCGACCCAGACACGACATCGTGCTGACTGATGATGCGGCAACCGCTG 748

QY		281	UlyMeGtGlyAlaIaphenValleuAlyTyAspGluLeuLysValle	298
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RESULT 10				
LOCUS	BOV2TRANS	1349 bp	mRNA	linear
DEFINITION	Bovine ADP/ATP translocase T2 mRNA, complete cds.			MAM 12-AUG-1994
ACCESSION	M24103 J02845			
VERSION	M24103.1 GI:529416			
KEYWORDS	ADP/ATP translocase; translocase.			
SOURCE	Bos taurus (cow)			
ORGANISM	Bos taurus			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
	Bovidae; Bovinae; Bos.			
REFERENCE	1 (bases 1 to 1349)			
AUTHORS	Powell,S.J., Medd,S.M., Runswick,M.J. and Walker,J.E.			
TITLE	Two bovine genes for mitochondrial ADP/ATP translocase expressed differences in various tissues			
JOURNAL	Biochemistry 28 (2), 866-873 (1989)			
MEDLINE	89229093			
PUBMED	2540808			
COMMENT	On Aug 13, 1994 this sequence version replaced by:341114. Original source text: Bos taurus cDNA to mRNA.			
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ORIGIN				
Alignment Scores:				
Pred. NO.:	1.84e-141	Length:	1349	
Score:	1512.00	Matches:	291	
Percent Similarity:	98.99%	Conservative:	4	
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Query Match:	97.99%	Indels:	0	
DB:	4	Gaps:	0	
US-09-811-094-33 (1-298) x BOV2TRANS (1-1349)				
QY	1	MetThGtGtGlnAlaIaIleSerPheAlaLysAspHeuAlaGlyGlyIleAlaAlaIa	20	
Db	64	ATGAGGAACAGGCCCATCTCCCTGCCAACAGATTCTCGGCCGGGCATCGCCGCC	123	
QY	21	IleSerLyTPHrAlaValAlaProIleGluArgValLysIleuDeuGlInVaIGnHis	40	
Db	124	ATCTCCAAGACTGGCGTGGCCCGCATCGAGCGGCGTCAAGCTCTGTCGACGTACAG	183	
QY	41	AlMetLySGlnIleAlaIaAspLysGlnIlyrLySGlYlleValAspCySIlleValArg	60	
Db	184	GCAAGACACACAGTCGGCCCGACAGACAAGCATGTAAGGCGATCGTAGCTGTCGCT	243	
QY	61	IleProLySGlnGlnGlyValIleuSerPheThrArgLyAsnIleuAlaSnValIleArg	80	
Db	244	ATCCCCAAGACACAGCGGCGTGCTGTCTTTGCGGGGCGAACTGTGCCCAAAGTCACTCG	303	
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[illegible]

[illegible]

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Db	730	CAGTCAGGACGCCAAGAAGAGCTGATATCATGTATCTGTGAGACATTTGACTGCTGGCGGAAG	789
QY	261	IlePhearGAspGIuGIyGIyLysAlaPhePheIysGIyAlaTrpSerAsnValIeuarG	280
Db	790	ATTCCAGAGGATGATGAGGAGGAGGAACGCTTCTTCAGAGGTGCATGGCTTAAATGTTCTCAGA	849
QY	281	GIyMetGIyGIyAlaPheValIeValIeuYrAspGIuIleuGIyLysValIle	298
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RESULT 12			
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DEFINITION	Sequence 2 from Patent WO0132876.		
ACCESSION	AX134719		
VERSION	AX134719.1		
KEYWORDS	GI:14271236		
SOURCE			
ORGANISM	Homo sapiens (human)		
REFERENCE	Homo sapiens		
AUTHORS	Eukarya; Eutheria; Primates; Catarrhini; Homidae; Homo.		
TITLE	Murphy, A.N., Clevenger, W., Wiley, S.E., Andreyev, A.Y., Filiger, L.G., Velicelebi, G. and Davis, R.E.		
JOURNAL	Compositions and methods for determining interactions of mitochondrial components, and for identifying agents that alter such interactions		
FEATURES	Patent: WO 0132876-A 2 10-MAY-2001; MITOKOR (US)		
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Score:	1454.00	Matches:	274
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Query Match:	94.23%	Indels:	0
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US-09-811-094-33 (1-298) x AX134719 (1-897)			
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QY	21	IleSerYrThrAlaValAlaProIleGIuArGIyAlaIysIleuIleuGIuAlaGlnHis	40
Db	61	ATCTCCAGAGCGGGGTAGCGCCCATCGAGCGGGGTCAAGCTCTGTGAGGTGACGAT	120
QY	41	AlaSerYrGlnIleAlaAlaAspYrGIuYrGIyGIyIleValAlaSpCysIleValArg	60
Db	121	GCCACCAAGCATCATCTGACATATAGCAATCAAAAGCATATATGACGCTGGTCCGT	180
QY	61	IleProlYrGIuGIuGIyAlaIleuSerPheTrpArgGIyAsnIleuAlaAsnValIleArg	80
Db	181	ATTCACAGGACACGAAATCTGTGCTTCTGGCGGGGTACCTGGCCAAATGCATCACA	240
QY	81	TyrPheTrpThrGlnAlaIleuAsnPheAlaPheYrAspYrGIyGIyGlnIlePheIleu	100
Db	241	TACTTCCCGACCCAGAGCTTAACTTCGGCTTCAAAAGATAAATATACAGCATCTTCCG	300
QY	101	GIyGIyAlaAspYrHisIstHrGlnPheTrpArgYrYrPheAlaGIyAsnIleuAlaSerGIy	120

Db 301 GGTGGTGTGACAGAGACACCAAGTTTGGCCGCTACTTGGCGGGAATCTGGCATCGGGT 360
OY 121 GYALAAAGAGLYAATrSerLeuCySPheValTYrProLeuAspPheAlaArgTYrArg 140
Db 361 GGTGGCGAGGGGACACATCCCTGTGTTGTGTACCTCTTGATTTTGGCCGATACCGGT 420
OY 141 LeuAlaAlaAspValGlySerGlyTYrThrGluArgGluPheArgGlyLeuGlyAspCys 160
Db 421 CTAGCACTGTATGTGGGTAAAGCTGAGCTGAAGGAAATTCAGAGCTGGGTGATGTC 480
OY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTYrGlnGlyPheSerValSer 180
Db 481 CTGGTTAAGATCTCAAAATCTGATGGATTAAGGCTGTACCAAGGCTTTAACTGTCT 540
OY 181 ValGlnGlyIleIleIleTYrArgAlaAlaTYrPheGlyValTYrAspThrAlaLysGly 200
Db 541 GTGCGGGTATATATCATCTACCGAGCGGCTACTGCTGATCTATGACACTGCAAGGA 600
OY 201 MetLeuProAspProLysAsnThrHisIleValAlaSerTPMetIleAlaGlnThrVal 220
Db 601 ATGCTTCGGATCCCAAGAACTCATCATGCTACCTGATGATGATGATGATGATGATG 660
OY 221 ThrAlaValAlaGlyValAlaSerTYrProPheAspThrValAlaArgArgMetMet 240
Db 661 ACTGCTGTGGCGGGGTGACTCTCTATCCATTTGACACCGTTCCGCCCGCATGATGATG 720
OY 241 GlnSerGlyArgLysGlyAlaAspIleMetTYrThrGlyThrValAlaAspCysTrpArgLys 260
Db 721 CAGTCAGGGGCGCAAGAGAACTGATCATCATGACAGGACGCTGTGCTGCTGGGGAAG 780
OY 261 IlePheArgAspGluGlyLysAlaPhePheLysGlyAlaTrpSerAsnValIleuArg 280
Db 781 ATTGCTGTGATGATGAAGAGCAAGCTTTTTCAGAGGCTGATGCTCATGTCTTCACA 840
OY 281 GlyMetGlyGlyAlaPheValIleuValLeuTYrAspGlyLeuLysLys 296
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RESULT 13
AX301847 897 bp DNA linear PAT 30-NOV-2001
LOCUS AX301847
DEFINITION Sequence 2 from Patent WO0185944.
ACCESSION AX301847
VERSION AX301847.1 GI:17382904
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Anderson, C.M., Davis, R.E., Clevenger, W., Willey, S.E., Miller, S.W., Szabo, T.R., Ghosh, S.S., Moos, W.H., Pal, Y., and Carroll, A.K.
TITLE Production of adenine nucleotide translocator (ant), novel ant ligands and screening assays therefor
JOURNAL Patent: WO 0185944-A 2 15-NOV-2001;
MITOKOR (US)
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source 1. 897
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
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BASE COUNT 209 a 223 c 246 g 219 t
ORIGIN

Alignment Scores:
Pred. No.: 6.87e-136 Length: 897
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Percent Similarity: 96.96% Conservative: 13
Best Local Similarity: 92.57% Mismatches: 9
Query Match: 94.23% Indels: 0
Gaps: 0

US-09-811-094-33 (1-298) x AX301847 (1-897)

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OY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTYrLysGlyIleValAlaPcySileValArg 60
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OY 121 GYALAAAGAGLYAATrSerLeuCySPheValTYrProLeuAspPheAlaArgTYrArg 140
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RESULT 14
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LOCUS HUMANPc
DEFINITION Human ADP/ATP carrier protein mRNA, complete cds.
ACCESSION J02683
VERSION J02683.1 GI:179246
KEYWORDS ADP/ATP carrier protein.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 (bases 1 to 1228)

AUTHORS Battini, R., Ferrari, S., Kaczmarek, L., Calabretta, B., Chen, S.T. and Basegga, R.

TITLE Molecular cloning of a cDNA for a human ADP/ATP carrier which is growth-regulated

JOURNAL MEDLINE J. Biol. Chem. 262 (9), 4355-4359 (1987)

PUBMED 8716606

COMMENT 3031073

Original source text: Human SV40 transformed fibroblast, cDNA to mRNA, clone hp2F1.

Draft entry and computer-readable sequence for [1] kindly provided by R. Battini, 09-MAR-1987.

The steady state levels of the ADP/ATP carrier mRNA are growth-regulated. They increase when quiescent cells are stimulated by serum, platelet-derived growth factor (PDGF), or epidermal growth factor (EGF), but not by platelet-poor plasma or insulin. mRNA levels of the ADP/ATP carrier decrease when growing H1-60 cells are induced to differentiate by either phorbol esters or retinoic acid.

FEATURES

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BASE COUNT 298 a 302 c 304 g 324 t

ORIGIN Unreported.

Alignment Scores:

Pred. No.: 1.02e-135 **Length:** 1228

Score: 1454.00 **Matches:** 274

Percent Similarity: 96.96% **Conservative:** 13

Best Local Similarity: 92.57% **Mismatches:** 9

Query Match: 94.23% **Indels:** 0

Gaps: 0

US-09-811-094-33 (1-298) x HUMATPC (1-1228)

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DB 130 ATCTCCAAAGCGGGGTAGCGCCATCGACGGGCTCAAGCTGCTGCGAGGTCACAT 189

QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAlaPcySIIleValArg 60

DB 190 GCGAGCAAGCAAGTCACTGAGATTAAGCATACAAAGCCATTATAGACTCGGGTCCGT 249

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DB 250 ATTCCTCCAAAGGAGCAAGAGTTCCTGCTTCGCGCGGTAACTGGCCATGTCATCAGA 309

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QY 101 GlyIValAspLysHisThrGlnPheTyrPArgTyrPheAlaGlyLysLeuAlaSerGly 120

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QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160

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QY 261 IlePheArgAspGluGlyLysAlaPhePheLysGlyValAlaThrSerAsnValLeuArg 280

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DB 910 GGCATGGCGTGTCTTTGTGCTTGTGCTTGTATGATGAATCAAGAAG 957

RESULT 15

AB065433

LOCUS Bos taurus mRNA for adenine nucleotide translocator 2, complete

DEFINITION

ACCESSION AB065433

VERSION AB065433.1 GI:18642495

KEYWORDS

SOURCE Bos taurus (cow)

ORGANISM Bos taurus

REFERENCE

AUTHORS Yamazaki, N., Shinohara, Y., Tanida, K. and Terada, H.

TITLE Structural properties of mammalian mitochondrial ADP/ATP carriers: identification of possible amino acids that determine functional differences in its isoforms

JOURNAL Mitochondrion 1, 371-379 (2002)

REFERENCE 2 (bases 1 to 1146)

AUTHORS Yamazaki, N., Shinohara, Y. and Tanida, K.

TITLE Direct Submission.

JOURNAL Submitted (11-JUL-2001) Naoshi Yamazaki, University of Tokushima, Faculty of Pharmaceutical Sciences, Stomach, Tokushima, Tokushima 770-8505, Japan (E-mail: yamazaki@fc.ph.tokushima-u.ac.jp, Tel: 81-88-653-7279)

FEATURES

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Thu Aug 28 08:34:55 2003

us-09-811-094-33.p2n.rge

Page 14

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: August 27, 2003, 05:30:34 ; Search time 334 Seconds

(without alignments)
2408.481 Million cell updates/sec

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Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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and is derived by analysis of the total score distribution.

SUMMARIES

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4	1543	100.0	1212	22	AA158797	Human polynucleoti
5	1543	100.0	2035	22	AA160583	Human polynucleoti
6	1510	97.9	2592	25	ABX63152	Human cDNA #152 d1
7	1463	94.8	1225	24	AA148635	Human insulin rece
8	1454	94.2	897	21	AAD00520	Human adenine nucl
9	1454	94.2	897	22	AA0505902	Human adenine nucl
10	1454	94.2	897	24	AA016689	DNA encoding human
11	1424	92.3	1196	24	ABX63420	Rat sequence diffe
12	1418	91.9	2213	25	ACC46652	Human dltup organe
13	1417	91.8	1156	23	AA091243	DNA encoding novel
14	1412	91.5	1177	19	AAV36479	Anti cDNA. Mus sp
15	1405	91.1	1259	19	AAV36480	Anti cDNA. Mus sp
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17	1385.5	89.8	894	22	AA0505901	Human adenine nucl
18	1385.5	89.8	894	24	AA016688	DNA encoding human
19	1385.5	89.8	1024	25	ABX83302	Toxicologically re
20	1385.5	89.8	1320	24	ABX65029	Invertebrate forag
21	1356.5	87.9	1116	24	ABX83761	Human cDNA diffe
22	1356.5	87.9	1116	24	ABN95598	Gene #2096 used to
23	1356.5	87.9	1116	24	AB169347	Prostate cancer re
24	1254.5	81.3	1581	23	AB118531	Drosophila melanog
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33	1119	72.5	1781	24	AD033664	Human TRICH-19 cDN
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36	1081	70.1	687	24	ABQ56282	DNA encoding novel
37	1043.5	67.6	3406	23	AB103126	Human ovarian anti
38	981	63.6	669	23	AB103126	Drosophila melanog
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44	796	51.6	943	24	ABN74319	Human colon cancer
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ALIGNMENTS

RESULT 1
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AAD00521 standard; cDNA: 897 BP.
ID
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AC AAD00521;
XX
DT 29-AUG-2000 (first entry)
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DE Human adenine nucleotide translocator ANT3 cDNA.
XX
KW Human; adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP;
KW adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
KW mitochondrial permeability transition; neuroprotective; neurologic;
KW antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
KW antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
KW antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
KW diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;

XX Claim 1: SEQ ID NO 1000; 10078bp; English.
 PS
 CC The invention relates to human nucleic acids (AA157798-AA161369) and
 CC the encoded polypeptides (AA158642-AA162213) with nootropic,
 CC immunosuppressant and cytoskeletal activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localized neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC Actin/Inhibin activity, Chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
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 SQ Sequence 1212 BP; 247 A; 395 C; 356 G; 214 T; 0 other;

Alignment Scores:
 Pred. No.: 2 48e-172 Length: 1212
 Score: 1543.00 Matches: 298
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
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 DB: 22 Gaps: 0

US-09-811-094-33 (1-298) x AA158797 (1-1212)

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 ID AA160583 standard; cDNA; 2035 BP.

AC AA160583;
 DT 22-OCT-2001 (first entry)
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 DE Human polynucleotide SEQ ID NO 4572.

XX Human; nootropic; immunosuppressant; cytoskeletal; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia; ss.

OS Homo sapiens.
 PN MO200153312-A1.
 XX

PD 26-JUL-2001.
 XX

PF 26-DEC-2000; 2000MO-US34263.
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PR 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-0552317.
 PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.
 XX

PA (HYSE-) HTSEQ INC.
 XX

PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac R;
 XX

DR WPI; 2001-442253/47.
 DR P-PSDB; AAA41427.
 XX

PT Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -
 XX

PS Claim 1: SEQ ID NO 4572; 10078bp; English.
 XX

CC The invention relates to human nucleic acids (AA157798-AA161369) and
 CC the encoded polypeptides (AA158642-AA162213) with nootropic,
 CC immunosuppressant and cytoskeletal activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC system, such as peripheral nervous injuries, peripheral neuropathy and

localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: immune system suppression, activation/inhibition of activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.

Note: The sequence data for this patent did not form part of the printed specification.

Sequence 2035 BP; 398 A; 611 C; 625 G; 401 T; 0 other;

Alignment Scores:
 Pred. No.: 5,12e-172 Length: 2035
 Score: 1543.00 Matches: 298
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 Gaps: 0

US-09-811-094-33 (1-298) x AA160583 (1-2035)

OY 1 MetThrGluGlnAlaIleSerPheAlaTyAspPheLeuAlaGlyIleAlaAla 20
 DB 1932 ATGAGGGAAGAGCCATCTCTCGCCAAAGACTTCTTGCCGAGGATCGCCGCC 1873
 OY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
 DB 1872 ATCTCAAGAGCGCGCTCGCATCGAGCGGCTCAAGCTCTGCTCGACAGTCCAGC 1813
 OY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
 DB 1812 GCCAGCAACAGATCGCGCGCAGCAAGTACAGAGGATCGTGGATGTCTGCC 1753
 OY 61 IleProLysGluGlnGlyValLeuSerPheTyrArgGlyAsnLeuAlaAsnValIleArg 80
 DB 1752 ATCCCAAGAGAGCGGCTCTCTCTCTGAGGCGCAACCTTGCCACAGTATTCGC 1693
 OY 81 TyrPheProThrGlnAlaIleuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
 DB 1692 TACTTCCCACTCAAGCCCTCACTTCCCTTCAAGATTAATACAGACATCTTCTCG 1633
 OY 101 GlyIleValAspLysHisThrGlnPheTyrArgGlyAsnLeuAlaSerGly 120
 DB 1632 GGGGGGTGACAGACAGCAGAGTCTGGAGTCTTGGCGGACCTGGCTCGGC 1573
 OY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
 DB 1572 GGTCCCGCCCGCGACCTCCCTGCTGCTGATGCCGATTTGCCAGAACCCGC 1513
 OY 141 LeuAlaAlaAspValGlyLysSerGlyTyrGluArgGluPheArgGlyLysGlyAspCys 160
 DB 1512 CTGCGACCGGACGTGGGAAAGTCAAGCAGACAGCGGAGTCCGAGGCTGGAGACTGC 1453
 OY 161 LeuValLysIleThrLysSerAspCylIleArgIleuTyrGlnGlyPheSerValSer 180
 DB 1452 CTGCTGAAGATCACCAAGTCCAGCGCATCCGGGCGCTGTACACAGGCTTCAGTGTCC 1393
 OY 181 ValGlnIleIleIleIleTyrArgAlaAlaLysPheGlyValTyrAspThrAlaLysGly 200
 DB 1392 GTGAGGAGCATCATCTACCGGGCGCATTCGCGCTGTACATCGCGCCAAAGGC 1333
 OY 201 MetLeuProAspProLysAsnThrHisIleValAlaSerTyrMetIleAlaGlnThrVal 220
 DB 1332 ATGCTCCCAACCCCAAGAACGACGACATCTGTGTGATGATGATCCGACAGACCTG 1273
 OY 221 ThrAlaValAlaGlyValAlaSerTyrProPheAspThrValArgTyrMetMetMet 240
 DB 1272 ACGGCGGCGCGCTGTCTTCAACCTTCACACAGGTGGGGGCGCATGATGATG 1213
 OY 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspTyrTrpArgLys 260

DB 1212 CAGTCCGGCGCCAAAGAGCTGACATCATGTACACGGCGACGCTGACTGTGAGGAAG 1153
 OY 261 IlePheArgAspGluGlyLysAlaPhePheLysGlyAlaTyrPheAsnValIleArg 280
 DB 1152 ATCTTAGAGATGAGGGGCGCAAGGCTTCTTCAAGGCTGCTGTCAACGTCTCGCG 1093
 OY 281 GlyMetGlyIleAlaPheValLeuValLeuTyrAspGluLeuLysValIle 298
 DB 1092 GGCATGGGGGCGCTGTGCTGTCTGTACAGACTCTCAAGAGTATC 1039

RESULT 6

ABX63152 standard; cDNA; 2592 BP.

ABX63152;

25-FEB-2003 (first entry)

Human cDNA #152 differentially expressed in activated vascular tissue.

Human; gene; ss; vascular tissue; cytosolic; atherosclerosis;
 cardiact; hypertensive; antidiabetic; gynaecological; vasculoprotective; gene therapy; vascular disease; cancer; coronary;
 artery disease; hypertension; diabetes; pre-eclampsia; restenosis;
 ischaemia; reperfusion injury; stroke;

Homo sapiens.

US2002137081-A1.

26-SEP-2002.

08-JAN-2002; 2002US-0044090.

28-JUL-2000; 2000US-222469P.

08-JAN-2001; 2001US-260483P.

(BAND/) BANDMAN O.

Bandman O;

WPI; 2003-110597/10.

Combination for diagnosing, staging, treating, or monitoring the progression of treatment of a vascular disease, e.g. atherosclerosis, comprises several cDNAs that are differentially expressed in activated vascular tissue -

Claim 1; Page -; 18pp; English.

This invention relates to a combination comprising several cDNAs that are differentially expressed in activated vascular tissue. The invention also discloses a high throughput method for detecting differentially expressed cDNAs in a sample. The cDNAs of the invention may have antiatherosclerotic, cytosolic, cardiact, hypertensive, antidiabetic, gynaecological, vasculoprotective and cerebroprotective activities and may be used in gene therapy. The cDNAs of the invention may be used in a high-throughput method for detecting differential expression of one or more cDNAs in a sample, or screening several molecules or compounds to identify a molecule or compound that specifically binds a cDNA of the invention. A protein encoded by the cDNA may be used to screen several molecules or compounds to identify a ligand that specifically binds to the protein, or to produce or purify an antibody to the protein that can be used to detect a protein in a sample or purify a natural or recombinant protein from a sample. The nucleotides may be useful for diagnosing, staging, treating, or monitoring the progression of a disease, e.g. atherosclerosis, diabetes, pre-eclampsia, ischaemia, artery disease, hypertension, diabetes, cancer, coronary artery disease, reperfusion injury, restenosis, or stroke. The cDNAs can also be used for large-scale genetic or gene expression analysis of several new nucleic acid molecules. Antibodies to the proteins encoded by the cDNAs are useful for diagnosing pre-pathologic disorders, and chronic or acute diseases associated with abnormalities in the expression.

CC amount or distribution of the protein. The present sequence
CC represents a cDNA of the invention that is differentially expressed in
CC activated vascular tissue.
CC Note: The sequence data for this patent did not form part of the
CC specification, but was obtained in electronic format directly from USPRO
CC at <http://seqdata.uspro.gov/sequence.html?docid=20020137081>.

XX Sequence 2592 BP: 520 A; 790 C; 766 G; 514 T; 2 other:

Alignment Scores:

Pred. No.:	5,72e-168	Length:	2592
Score:	1510.00	Matches:	296
Percent Similarity:	99.33%	Conservative:	2
Best Local Similarity:	98.67%	Mismatches:	0
Query Match:	97.86%	Indels:	2
DB:	25	Gaps:	0

US-09-811-094-33 (1-298) x ABX63152 (1-2592)

```
OY 1 MetThrgluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyIle-AlaAlaAl 20
DB 207 ATGACGAAACAGGCGCATCTCTCGCCAAAGACTTCTGGCGGAGCATGGCGCGCCG 266
OY 20 aIleSerIysThrAlaValAlaProIleGluArg-ValIlyLeuLeuGlnValGlnH 40
DB 267 CATCTCCAAAGCGCGCGTCTCGATCGACGGGGGTCACGCTGCTGCAGGTCAGC 326
OY 40 lAlaSerIysGlnIleAlaAlaLysAspIysGlnIlyLeValaIspCysIleVala 60
DB 327 ACGGCAAGCAAGATCGCCCGCCGCAAGCGGTACAAAGGCGTGGAGTGCATTTGCC 386
OY 60 rGlieProIysGluGlnIlyValleuSerPheTrpArgIlyAsnLeuAlaValIlea 80
DB 387 GCATCCCAAGAGAGAGCGCGTCTGCTCTTGAGGGGCAACCTTGCAACGTCATTC 446
OY 80 rGlyTrpPheProThGlnAlaLeuAsnPheAlaPheLysAspIysIlysgIlePheL 100
DB 447 GCTACTTCCCACTCAAGCCCTCAACTTCGCTTCAAGAAATGACAGAGATCTTCC 506
OY 100 euGlyIlyValaIspIysIsthTrgInPheTrpArgIlyPheAlaGlyAsnLeuAlaSerG 120
DB 507 TGGGGGGGTGGACAAAGCAAGCAAGTCTGAGAGTACTTTGGGGCAACCTGGCTCG 566
OY 120 lylGlyAlaAlaGlyAlaThrSerIeucysPheValIlyrProLeuAspPheAlaArgThra 140
DB 567 GCGGTGCGCGCGCGGCGACTCCCTCTGCTTGTACCGGCTGATTTTGGCAACAACC 626
OY 140 rGleuAlaAlaAspValGlyIysSerGlyThrGluArgGluPheArgGlyLeuGlyAspC 160
DB 627 GCGTGGCGGAGCGACTGGGAAAGTCAAGCAGACGCGAGATTCGAGGCGCTGGAGACT 686
OY 160 lylLeuValIysIleThrIysSerAspGlyIleArgGlyLeuTrgIingIlyPheSerValS 180
DB 687 GCCTGTGTAAGATCCCAAGTCCGACGCGATCCGGGCTCTTACCAAGGGCTTCACTGT 746
OY 180 erValGlnGlyIleIleIleIlyrArgAlaAlaIytrPheGlyValIlyrAspThrAlaIysG 200
DB 747 CCGTGCAGGGCATCATCATACCGGGCGGCTACTTGGCGGTACGATACGATGCGCAAG 806
OY 200 lylMetLeuProAspProIysAsnThrHisIleValIleValIserTrpMetIleAlaGlnThrv 220
DB 807 GCATGCTCCCGACCCCAAGAACAGCAGCATCTGTGTAAGCTGATGATTCGCGAGACCG 866
OY 220 aIThrAlaValAlaGlyValIserIlyrProPheAspThrValIArgTrgArgMetMetI 240
DB 867 TGACGGCGCTGGCGCGCTGTGTCTTACCCCTTGACACGGTGGGGGCGCCATGATGA 926
OY 240 etGlnSerGlyrArgIysGlyAlaAspIleMetIlyrThrGlyThrValaIspCysIlyrParG 260
DB 927 TGCAGTCCGGGGCAAGAGAGCTGACATCATGTACAGGGGCGCTGCAGCTTTGGAGGA 986
OY 260 yslIlePheArgAspIleGlyIlyrAlaIlePhePheLysGlyAlaTrpSerAsnValLeuA 280
```

```
DB 987 AGATCTTCAGAGATGAGGGGGGCAAGGCGCTTCTTCAAGGGTGGCTGCCAAGCTCTGC 1046
OY 280 rGlyMetGlyIyAlaIlePheValIleuValIleuTyraSPGluLeuIysIlyValIle 298
DB 1047 GGGGCGATGGGGGCGCGCTTCTGCTGTGTCTGTACGACGAGCTCAAGAAAGGTGATTC 1102

RESULT 7
AAL48635
ID AAL48635 standard; cDNA; 1225 BP.
XX
XX AC AAL48635;
XX
XX DT 11-OCT-2002 (first entry)
XX
XX DE Human insulin receptor signaling modifier cDNA SEQ ID NO: 53.
XX
XX KW Human; insulin receptor signaling; insulin receptor signaling modifier;
XX ISM; diabetes; metabolic syndrome; antidiabetic; gene; ss.
OS Homo sapiens.
XX
XX PN WO200255664-A2.
XX
XX PD 18-JUL-2002.
XX
XX PF 11-JAN-2002; 2002WO-US01048.
XX
XX PR 12-JAN-2001; 2001US-261226P.
XX PR 12-JAN-2001; 2001US-261303P.
XX PR 12-JAN-2001; 2001US-261304P.
XX PR 12-JAN-2001; 2001US-261335P.
XX PR 12-JAN-2001; 2001US-261336P.
XX PR 12-JAN-2001; 2001US-261361P.
XX PR 12-JAN-2001; 2001US-261456P.
XX PR 12-JAN-2001; 2001US-261457P.
XX PR 12-JAN-2001; 2001US-261458P.
XX PR 12-JAN-2001; 2001US-261459P.
XX PR 12-JAN-2001; 2001US-261461P.
XX PR 12-JAN-2001; 2001US-261518P.
XX PR 12-JAN-2001; 2001US-261531P.
XX PR 12-JAN-2001; 2001US-261532P.
XX PR 12-JAN-2001; 2001US-261589P.
XX PR 12-JAN-2001; 2001US-261590P.
XX PR 12-JAN-2001; 2001US-261594P.
XX PR 12-JAN-2001; 2001US-261695P.
XX PR 12-JAN-2001; 2001US-261697P.
XX
XX PA (EXEL-) EXELIXIS INC.
XX
XX PI Setdel-Dugan C, Ferguson KC, Kidd T;
XX
XX DR WPI: 2002-599664/64.
XX P-PSDB; AAO18516.
XX
XX PT Identifying an insulin receptor signaling modulator, useful as drug
XX PT targets for treating diabetes or metabolic disorders, comprises
XX PT contacting an assay system comprising insulin receptor signaling
XX PT modifiers with a test agent
XX
XX PS Disclosure: Page 159-160; 232pp; English.
XX
XX
XX The present invention relates to a method of identifying a candidate
XX insulin receptor (INR) signaling modulating agent, involving contacting
XX an assay system comprising an insulin receptor signaling modifier (ISM)
XX polypeptide or nucleic acid with a test agent, and detecting a test
XX agent-biased activity of the assay system. The method is useful for
XX identifying candidate INR signaling modulating agents. ISM genes may be
XX used as drug targets for treatment of disorders related to INR signaling
XX such as diabetes or metabolic syndrome. ISM nucleic acids and
XX polypeptides are useful for identifying and testing agents that modulate
XX ISM function and for other applications related to the involvement of ISM
XX in INR signaling, and for identifying subjects having a predisposition to
XX such diseases associated with INR signaling. The present sequence is an
```

CC ISM coding sequence described in the exemplification of the invention
XX
SQ Sequence 1225 BP; 295 A; 300 C; 307 G; 323 T; 0 other;

Alignment Scores:		
Pred. NO.:	7.18e-163	length: 1275
Score:	1663.00	Matches: 275
Percent Similarity:	97.908	Conservative: 13
Best Local Similarity:	92.918	Mismatches: 0
Query Match:	94.828	Indels: 0
DB:	24	Gaps: 0

US-09-811-094-33 (1-298) x AAL48635 (1-1225)

[illegible]

RESULT 8	
AAD00520	
ID	AAD00520 standard; cDNA; 897 BP.

AC AAD00520;

DT 29-AUG-2000 (first entry)

Human adenine nucleotide translocator ANT2 cDNA

KM Human; nemaline nucleotide transferase; AN2; mitochondrial; ADP; ATP;
KM adenosine tri-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
KM mitochondrial permeability transition; neuroprotective; neurotrophic;
KM antiparisonam; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
KM antipsychotic; cerebroprotection; therapeutic; screening; psoriasis;
KM Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
KM diabetes; Leber's hereditary optic neuropathy; stroke; MIND;
KM mitochondrial encephalopathy; lactic acidosis; schizophrenia; MELAS;
KM mitochondrial diabetes and deafness; hyperproliferative disorder;
KM myoclonic epilepsy red ragged fibre syndrome; ss.

aa Homo sapiens.

AA	Key	Location/Qualifiers
FH		

```

E1      CDS      11001
ET      /*tag= a

```

AA WO200026370-A2
PN

AA PD 11-MAY-2000

XX 03-NOV-1999; 99WO-US25883.
PF

XX
PR 03-NOV-1998; 98US-0185904.

08-SEP-1999; 0905-033344.1
PK
XX

PA (M.I.U-) M.I.UOK-
XX

PI Anderson CM,	Davis RE,	Cleveland W,	Wiley CJ,	Harmon CM,	Shaw JH,	Wiley CJ,	Harmon CM,	Shaw JH,
PI Ghosh SS,								

XX
DR WPT: 2000-365619/31.

DR P-PSDB; AAY/1032.
XX

polypeptide, useful e.g. in screening for potential therapeutic agents

PT against mitochondrial disease -
XX

PS Example 1: Page 105-106; 1/3pp; Amg,15m.

XX

CC The patent discloses a method to produce adenine nucleotide translocator

CC (ANT) proteins or ANT fusion proteins using recombinant expression

CC constructs. ANT is a nuclear encoded protein and a major component of

CC inner mitochondrial membrane. It mediates transport of adenosine

CC diphosphates across the mitochondrial inner membrane and also serves

CC as an important molecular component of the mitochondrial permeability

CC transition pore, a modulator of apoptosis. ANT is used to identify agent

CC or ligands that bind to, or interact with it. The ANT ligands are used to

CC detect or isolate ANT in a biological sample, and therapeutically for

CC regulating mitochondrial pore activity, for treating diseases associated

CC with altered mitochondrial function, including Alzheimer's, Parkinson's

CC and Huntington's diseases, cancer, porcelias, diabetes, dystonia,

CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial

CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative

CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic

CC epilepsy red ragged fibre syndrome. The present sequence is a cDNA

CC encoding adenine nucleotide translocator ANT2 from human brain.

XX Sequence 897 BP; 209 A; 223 C; 246 G; 219 T; 0 other
50

Alignment Scores:

Pred. No.: 5,37e-162 Length: 897
 Score: 1454.00 Matches: 274
 Percent Similarity: 96.96% Conservative: 13
 Best Local Similarity: 92.57% Mismatches: 9
 Query Match: 94.23% Indels: 0
 DB: 21 Gaps: 0

US-09-811-094-33 (1-298) x AAD00520 (1-897)

QY 1 MetThrGlnGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyIleAlaAla 20
 DB 1 ATGACAGATGCCGATGTCCTTCGCCAAGGACTTCTGCGACGTGAGTGGCCGAGCC 60
 QY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnAlaGlnHis 40
 DB 61 ATCTCCAGACGGCGGTAGCGCCCATCGAGCGGCTGAGTGTGCTGCAGGTGCAGCAT 120
 QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
 DB 121 GCCAGCAGACGAGTCACTGCAATAGCAATACAAAGGCAATATAGACTGCGTCCGT 180
 QY 61 IleProLysGlnGlnIleValLysSerPheTyrPArgGlyAsnLeuAlaValIleArg 80
 DB 181 ATTCCTCAAGGACGAGAAATTCGTCTTCTGCGCGGTACCTGGCCCAATGTCATCAGA 240
 QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
 DB 241 TACTTCCACCCAGGCTCTTACTCTGCGCTTCAAAAGATTAATACAAAGAGATCTCC 300
 QY 101 GlyGlyValAspLysHisThrGlnPheTyrPArgTyrPheAlaGlnLysLeuAlaSerGly 120
 DB 301 GGTGGTGTGACACAAAGAAACCCGATTGTGGCGTACTTGCACAGGAAATCGCATCGG 360
 QY 121 GlyAlaAlaGlyValaThrSerLeuGlyPheValTyrProLeuAspPheAlaArgThrArg 140
 DB 361 GGTGGCGGAGGGGCCATCCCTGTGTTTGTGTACCTCTGATTTTGCCCGTACCCGT 420
 QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
 DB 421 CTAGCAGCTGATGTGGTAAAGCTGAGGTGAAAGGAATTCGAGGCGCTGATGCTGC 480
 QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
 DB 481 CTGGTTAAATCTACAAATCTGTATGGATTAAGGCGCTGTACCAAGGCTTTTACGTC 540
 QY 181 ValGlnGlyIleIleThrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
 DB 541 GTCCAGGATATATCATCTACCGACGCCCTACTTGGTATCTATGACACTGCAAGGA 600
 QY 201 MetLeuProAspProLysAsnThrHisIleValIleSerTyrMetIleAlaGlnThrVal 220
 DB 601 ATGCTTCGCGATCCCAAGAACACTCATCTGATCAGCGATGATCGCACAGACTGC 660
 QY 221 ThrAlaValAlaGlyValIleSerTyrProPheAspThrValArgArgMetMetMet 240
 DB 661 ACGCTGTGGCCGGGTGACTCTTATCCATTTTGAACCGTTCGCCGCGCATGATGATG 720
 QY 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTyrPArgLys 260
 DB 721 CAGTCAGGCGCAAGGAACTGACATCATCTACACAGCAGCGTTGACTCTGCGGAG 780
 QY 261 IlePheArgAspGlnGlyLysAlaPhePheLysGlyAlaTyrPheSerAsnValLeuArg 280
 DB 781 ATGCTCTGTGATCAAGAGGCAAGGCTTTTTCAGAGGTGCATGTCATGTTCTCAGA 840
 QY 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGlnLeuLysLys 296
 DB 841 GGCATGGGTGGTCTTTGTGCTGTGTATGATGAATCAAGAG 888

RESULT 9
 AAS05902
 ID AAS05902 standard; cDNA; 897 BP.
 XX

AC AAS05902;
 XX 07-SEP-2001 (first entry)
 DT Human adenine nucleotide translocator-2 (ANT-2) cDNA sequence.
 XX
 XX Human; adenine nucleotide translocator-2; ANT-2; MPT; cyclophilin;
 KW mitochondrial permeability transition pore component; cell survival;
 KW mitochondrial core component; mitochondrial related disorder; cancer;
 KM Alzheimer's disease; diabetes mellitus; hyperproliferative disorder; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..897
 FT /tag- a
 FT /product- "ANT-2"
 XX
 PN W0200132876-A2.
 XX
 PD 10-MAY-2001.
 XX
 PF 03-NOV-2000; 2000MO-US30535.
 XX
 PR 03-NOV-1999; 99US-0434354.
 XX
 PA (MITO-) MITOKOR.
 XX
 PI Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Fritzer LG;
 PI Velicelel G, Davis RE;
 XX
 DR WPI; 2001-291054/30.
 XX
 DR P-PSDB; AAU01199.
 XX
 PT New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 PT fused to energy transfer molecule -
 XX
 PS Disclosure; Fig 1; 186pp; English.
 XX
 CC The present sequence encodes for human adenine nucleotide translocator-2
 CC (ANT-2) protein. ANT proteins are mitochondrial permeability
 CC transition (MPT) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cyclophilins to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
 CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
 CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,
 CC hyperproliferative disorders e.g. cancer, and deafness.
 XX
 SQ Sequence 897 BP; 209 A; 223 C; 246 G; 219 T; 0 other;

Alignment Scores:

Pred. No.: 5,37e-162 Length: 897
 Score: 1454.00 Matches: 274
 Percent Similarity: 96.96% Conservative: 13
 Best Local Similarity: 92.57% Mismatches: 9
 Query Match: 94.23% Indels: 0
 DB: 22 Gaps: 0

US-09-811-094-33 (1-298) x AAS05902 (1-897)

Db 181 ATCCCAAGAGCAGCAAGTTCTGTCCTTGGCCCGGTACCTGGCCCAAGTCAATCA 240
 Qy 81 TyrPheProthrglnAlaLeuansPhealaphelyAspLysTyrLysGlnIlePheLeu 100
 Db 241 TACTTCCCAACCCAGGCTTAACTGGCTTCAAAAGTAATACAGAGATCTTCTCG 300
 Qy 101 GilyGlyValAspLysHisThrGlnPheTparGlyTyrPheAlaGlyAsnLeuAlaSerGly 120
 Db 301 GGTGGTGTGACAAAGAGAACCCAGTTTGGCGCTACTTGTGACAGGAATCTGGCATCGGGT 360
 Qy 121 GlyAlaAlaGlyAlaThrSerLeuGlyPheValTyrProLeuAspPheAlaIargArg 140
 Db 361 GGTGGCGAGAGGGGCGCAACATCCCTGTGTTTGTGTACCCCTGTGATTTTGGCCGTACCCGT 420
 Qy 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
 Db 421 CTAGACAGTGAATGTGGTAAAGCTGAGCTGAAAGGAATTCAGAGGCTCGTGAATGTC 480
 Qy 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
 Db 481 CTGGTTAAGATCTACAAATCTGATGGATTAAGGCGCTGACCAAGGCTTAACTGTCT 540
 Qy 181 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
 Db 541 GTGCGAGGTATATATCTACCGAGCCGCTACTGCTGGTATCTATGACACTGCAGAGGGA 600
 Qy 201 MetLeuProAspProLysAsnThrHisIleValIleSerTyrMetIleAlaGlnThrVal 220
 Db 601 ATGCTCCGATCCCAAGACACTCACATCGTCAGTCAGTGTGATGTCACAGACTGTC 660
 Qy 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValIargArgIleMetMet 240
 Db 661 ACTGCTGTGCGGGGTGTGACTTCCATTCATTTGACACCGTTCGCGCGCATGTATGATG 720
 Qy 241 GlnSerGlyArgLysGlyAlaAlaSerIleMetTyrThrGlyThrValAspCysThrArgLys 260
 Db 721 CAGTACAGGCGCCAAAGAGCACTGACATCATGTACAGAGCACCTGACTGCGGGAAG 780
 Qy 261 IlePheArgAspGluGlyLysAlaPhePheLysGlyAlaTyrSerAsnValLeuArg 280
 Db 781 ATTGCTCGATGAGAGGAGGAGCAAGCTTTTTCAGAGGGTGCATGTCATGTTCTCAGA 840
 Qy 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLys 296
 Db 841 GGCATGGGTGTGCTTGTCTTGTCTGTATGATGAATCAAGAG 888
 RESULT 11
 ABR63420
 ID ABR63420 standard; cDNA; 1196 BP.
 AC ABR63420;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Rat sequence differentially expressed in response to a hepatotoxin #1327.
 XX
 KW Rat; ss; hepatotoxin; expressed sequence tag; EST; drug screening;
 XX differential expression; centrilobular necrosis; steatosis.
 OS Rattus norvegicus.
 XX
 PN WO200210453-A2.
 PD 07-FEB-2002.
 PF 30-JUL-2001; 2001WO-US23872.
 XX
 PR 31-JUL-2000; 2000US-222040P.
 PR 02-NOV-2000; 2000US-244880P.
 PR 11-MAY-2001; 2001US-290029P.
 PR 15-MAY-2001; 2001US-290645P.
 PR 22-MAY-2001; 2001US-292336P.
 PR 06-JUN-2001; 2001US-295798P.

PR 13-JUN-2001; 2001US-297457P.
 PR 19-JUN-2001; 2001US-298884P.
 PR 09-JUL-2001; 2001US-303459P.
 XX
 PA (GENE-) GENE LOGIC INC.
 XX
 PI Mendrick D, Porter MW, Johnson KR, Castle AL, Elashoff MR;
 DR WPI; 2002-241625/29.
 XX
 PT Predicting toxic effects of compounds or the progression of these toxic
 PT effects by determining the changes in gene expression in tissues or
 PT cells exposed to the toxin and comparing these to gene expression in
 PT unexposed tissues or cells
 PS
 XX
 PS Claim 1: Seq ID No 1327; 239pp; English.
 CC
 CC The invention relates to methods for predicting toxic effects of
 CC compounds or the progression of these toxic effects by determining the
 CC global changes in gene expression in tissues or cells exposed to the
 CC toxin and comparing these to gene expression in unexposed tissues or
 CC cells. Also included are methods of predicting at least one toxic
 CC effect of a compound or progression of a toxic effect, preferably the
 CC hepatotoxicity of a compound, comprising detecting the level of
 CC expression in a tissue or cell sample exposed to the compound of two or
 CC more genes listed in the specification, where differential expression of
 CC the genes is indicative of at least one toxic effect or progression.
 CC The method can also be used to identify an agent which modulates the
 CC toxic response and predict cellular pathways that a compound modulates
 CC in a cell. The methods utilize a set of at least two probes (on a solid
 CC support in kit form), where each of the probes comprises a sequence that
 CC specifically hybridises to a gene listed in the specification, a computer
 CC system comprising a database containing information identifying the
 CC expression level in a tissue or cell sample exposed to a hepatotoxin of a
 CC set of genes comprising at least two genes listed in the specification,
 CC and a user interface to view the information used to present information
 CC identifying the expression level in a tissue or cell of at least one gene
 CC listed in the specification. The method is useful for elucidating global
 CC changes in gene expression and for identifying toxicity markers in
 CC tissues or cell exposed to a known toxin. The genes may be used as
 CC toxicity markers in drug screening and toxicity assays. The genes and
 CC gene expression information may be used as diagnostic markers for the
 CC prediction or identification of the physiological state of tissue or cell
 CC sample that has been exposed to a compound or agent. Hepatotoxicity
 CC is characterised by centrilobular necrosis and steatosis. The present
 CC sequence is an expressed sequence tag (EST) or cDNA derived from a gene
 CC which is differentially expressed in response to a hepatotoxic agent.
 XX
 SQ Sequence 1196 BP; 295 A; 279 C; 326 G; 296 T; 0 other;
 Alignment Scores:
 Pred. No.: 2, 83e-158 Length: 1196
 Score: 1424.00 Matches: 267
 Percent Similarity: 95.648 Conservative: 18
 Best Local Similarity: 89.608 Mismatches: 13
 Query Match: 92.298 Indels: 0
 DB: 24 Gaps: 0
 US-09-811-094-33 (1-298) x ABR63420 (1-1196)
 Qy 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyLylleAlaAla 20
 Db 76 ATGGGGATCAGAGCTTGTGACTTCTTAAAGACTTCTGCGAGTGCAGCGCGCGC 135
 Qy 21 IleSerLysThrAlaValAlaProIleGluValLysLeuLeuLeuAlaGlnHis 40
 Db 136 GTCTCCAAAGCCGCGTCCGCCGATCGAGAGGGTCAAACTGCTGTCAGGTCCAGCAT 195
 Qy 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
 Db 196 GCGAGCAACAGATCAGTGCAGAGAAACGTCACAAAGCATATTCATGTGTGTGACGA 255
 Qy 61 IleProLysGluGlnGlyValLeuSerPheTparGlyLysLeuAlaAsnValIleArg 80

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Db      256 ATCCCAAGAGACGAGGCTTTCTCTCTCTCGAGAGGGGTACTGGCCAACTGATCCGG 315
QY      81 TyrPheProThrGlnAlaLeuAspPheAlaPheIleAspIleTyrIleGlnIlePheLeu 100
Db      316 TACTTCCCAACCAAGATCTCTCACTTCCCTTCAAGACAAAGATACAGAGATCTTCCG 375
QY      101 GlyIleValAspIlePheIleThrGlnPheThrArgIlePheAlaIleValAsnIleAspIle 120
Db      376 GAGAGTGGAGTCTGCTTACGATCTTGGGCTGCTTCTGCTGCTGCTGCTGCTGCTGCT 435
QY      121 GlyAlaAlaGlyAlaThrSerLeuAspIleValIleThrProLeuAspPheAlaIleThrArg 140
Db      436 GGGGCACTGGAGGCTTACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 495
QY      141 LeuAlaAlaAspValIleGlySerIleGlyThrGlnArgIlePheAlaIleGlyAspIle 160
Db      496 CTGGCTGGCAAGCGGCAAGGATCTTCCAGCGCTGATTCATGAGGCTGGGCTGCTGCT 555
QY      161 LeuValIleIleThrIleThrIleSerAspIleValIleGlyIleThrGlnIlePheSerVal 180
Db      556 CTACCAACCAATCTCAAGTCTGATGGCTGAGAGGCTCTCTACAGGCTTCACTGCTCT 615
QY      181 ValGlnGlyIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 200
Db      616 GTGCGGGGATCTCACTCTACAGCTGCTCTGAGTCTATGACACTGCTCAAGGGG 675
QY      201 MetLeuProAspProIleAsnThrIleValIleValIleSerIlePheIleAlaIleThrVal 220
Db      676 ATGCTCCCAAGCCCAAGATGTCACATTTATGTGACCTGATGATGGCCAGAGTGTG 735
QY      221 ThrAlaValAlaGlyValAlaSerIleProPheAspThrValIleArgIleGlyMetIle 240
Db      736 ACAGCCGAGGCGGAGGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 795
QY      241 GlnSerGlyValGlyGlyAlaAspIleMetIleThrGlnIleThrValAspIlePheIle 260
Db      796 CACTCTGGCGGAGAGGAGGCTGATTTATGTGACAGGAGGAGCTGCTGCTGCTGCTGCTG 855
QY      261 IlePheArgAspGlnIleGlyIleValAlaPhePheIleGlyAlaIlePheAsnValIle 280
Db      856 ATTCGCAAAAGATGAGAGGAGGCTTCTTCAAGGCTGCTGCTGCTGCTGCTGCTGCTG 915
QY      281 GlyMetGlyIleAlaPheValIleValIleValIleValIleValIleValIleValIle 298
Db      916 GGCATGGGGGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 969
RESURF 12
ID      ACC46652 standard; cDNA; 2213 BP.
AC      ACC46652;
XX      02-JUN-2003 (first entry)
DE      Human dithp organelle-associated protein-encoding cDNA.
XX      Human, dithp: diagnostic and therapeutic polynucleotide; diagnosis;
XX      cancer; cell proliferative disorder; autoimmune disorder;
XX      inflammatory disorder; infection; hormonal disorder; metabolic disorder;
XX      neurological disorder; gastrointestinal disorder; transport disorder;
XX      connective tissue disorder; drug screening; proteome analysis;
XX      gene therapy; antisense therapy; genotyping; transgenic animal; knock in;
XX      disease model; toxicological testing; transcript imaging;
XX      organelle-associated protein; gene; ss.
OS      Homo sapiens.
XX      WO200297031-A2.
XX      05-DEC-2002.
XX      27-MAR-2002; 2002W0-US10056.

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XX      28-MAR-2001; 2001US-279619P.
PR      29-MAR-2001; 2001US-280067P.
PR      29-MAR-2001; 2001US-280068P.
PR      16-MAY-2001; 2001US-291280P.
PR      17-MAY-2001; 2001US-291829P.
PR      17-MAY-2001; 2001US-291849P.
PR      19-JUN-2001; 2001US-299428P.
PR      20-JUN-2001; 2001US-299776P.
PR      20-JUN-2001; 2001US-300001P.
XX      (INCYTE GENOMICS INC.
PA      Daffo A, Jones AL, Tran AB, Dahl CR, Gletzen D, Chinn J,
PI      Dufour GE, Hillman JL, Yu JT, Tuason O, Yap PE, Amesey SR,
PI      Daugherty SC, Dan TC, Liu TF, Nguyen DA, Kleefeld T, Gerstin EH,
PI      Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SK, Harris B,
PI      Flores V, Marwaha R, Lo A, Lan RT, Urashka ME;
XX      WPI; 2003-129518/12.
DR      P-PSDB; ABR41715.
XX      Novel human diagnostic and therapeutic polypeptide useful for
PT      identifying test compound which specifically binds to a polypeptide
PT      encoded by human diagnostic and therapeutic polynucleotide, and to
PT      induce antibodies
XX      Claim 2; SEQ ID No 573; 591pp; English.
XX      The invention relates to novel human diagnostic and therapeutic
XX      polynucleotides designated dithp (ACC46080-ACC46749) and to their
XX      encoded proteins (DITHP; ABR41136-ABR41812). The invention also relates
XX      to polynucleotide sequences at least 90% identical to the dithp cDNA
XX      sequences of the invention; recombinant vectors, host cells and
XX      transgenic organisms comprising a dithp protein; antibodies specific for dithp
XX      proteins; microarrays comprising dithp nucleic acid sequences; methods
XX      of detecting dithp nucleotide and protein sequences; methods of
XX      assessing the toxicity of test compounds using a dithp protein; and
XX      a probe. Dithp nucleic acid sequences and dithp proteins may be used in the
XX      diagnosis of a wide variety of conditions including cancer and other cell
XX      proliferative disorders; autoimmune or inflammatory disorders; metabolic
XX      disorders; neurological disorders; gastrointestinal disorders; transport
XX      disorders; and connective tissue disorders. They may also be used to
XX      screen for modulators of protein activity or gene expression. DITHP
XX      proteins can additionally be used in analysis of the effects of a tissue
XX      or cell type and to induce antibodies. The dithp therapy of the disorders
XX      mentioned above, as a source of antisense sequences, a source of
XX      probes and primers, in genotyping and identification of individuals, in
XX      the generation of transgenic animal models of human disease or knock in
XX      humanised animals, in toxicological testing, and in transcript imaging.
XX      The present sequence represents a dithp cDNA encoding a DITHP protein
XX      which is an organelle-associated protein.
XX      Note: The sequence data for this patent did not form part of the printed
XX      specification, but was obtained in electronic format directly from MRO
XX      at ftp.wipo.int/pub/publ/published_pcl_sequences.
XX      Sequence 2213 BP; 422 A; 751 C; 633 G; 407 T; 0 other;
S0
Alignment Scores:
Pred. No.: 3,43e-157 Length: 2213
Score: 1418.00 Matches: 277
Percent Similarity: 96.22% Conservative: 3
Best Local Similarity: 95.19% Mismatches: 5
Query Match: 91.90% Indels: 5
DB: 25 Gaps: 2
US-09-811-094-33 (1-298) x ACC46652 (1-2213)
QY      1 MetThrGlnGlnAlaIleSerPheAlaIleSerPheAlaIleGlyIleAlaAlaAla 20

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Db      206 ATGACGAGAACAGCCATCTCTTCGCGCAAGACCTTCTTGCGGAGGCAATCGCGCGCC
Qy      21  IleserlysthrAlaValAlaProIleGluArgValIleLeuLeuGlnHis 40
Db      266 ATCTCCAGAGAGCGCGTGGCTCGATCGAGCGGCTCAACCTCTGTCGAGGTCGACGAC
Qy      41  AlaserlysglnIleAlaAlaAspIlysglnIleValAspCysIleValArg 60
Db      326 GCCAGCAGACAGATCGCCCGCAGCAAGCAGTACAAAGGCGATGAGCATGTCATTCGCC
Qy      61  IleProlysglnGlnGlyValIleuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80
Db      386 ATCCCGACAGAGAGCGCGTGGCTCTGAGGAGGCAACCTTCACCAAGCATTCGC
Qy      81  TyrPheProThrGlnAlaLeuAsnPheAlaPheIlyAspIlyTrpIlysglnIlePheLeu 100
Db      446 TACTTCCCGACACAGCCCTCAACTTCGCTTCAAGAGTAAGTACAGACAGATCTTCG
Qy      101 GilyGlyValAspIlyHisThrGlnPheTrpArgGlyPheAlaGlyAsnLeuAlaSerGly 120
Db      506 GGGGCGGTGGACAGACAGCAGATCTGAGGTACTTGGCGGCAACCTGGCCCTCGGC
Qy      121 GlyAlaAlaGlyAlaThrSerLeucysPheValIlyProLeuAspPheAlaArgThrArg 140
Db      566 GGTGGGCGCGCGCGACCTCCCTGCTGCTGCTGATCCCGTGGATTTCGCGAAGCCGC 625
Qy      141 LeuAlaAlaAspValGlyIlySerGlyThrGluArgGluPheArgIlyLeuGlyAspCys 160
Db      626 CTGGCAGCGGAGCTGGGAAGTCAGCAGCAGACAGCGGATTCGAGCGCTCGAGACTGC 685
Qy      161 LeuValIlyIleThrIlySerAspIlyIleArgGlyLeuIlyGlnIlyPheSerValSer 180
Db      686 CTGGTGAAGATACCAAGATCCAGCGGATCCGCGGCTTACCAAGGCTTCAGTGTCTCC 745
Qy      181 ValGlnGlyIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 200
Db      746 GTGCGAGGATCATCTTACCGGGGCGCTTCTGCGGTGATGATCGGCGCAAGGCG 805
Qy      201 MetLeuProAspProIlyAsnThrHisIleValIleSerTrpMetIleAlaGlnThrVal 220
Db      806 ATGCTCCCGGACCCCAAGAACAGCAGCATCGTGATGATGATGCCGCGAGACCGTG 865
Qy      221 ThrAlaValAlaGlyValIleSerIlyProPheAspThrValArgArgMetMet 240
Db      866 ACGGCGGTGGCGCGTGTCTCTACCCCTTCGACACGCTGGCGCGCATGATGATG 925
Qy      241 GlnSerGlyArgIlyGlyAlaAspIleMetIlyTrpGlyThrValAspCysTrpArgIly 260
Db      926 CAGTCCGGGCGCAAGAGACCTGACATCATCATACGCGGCAACCTGCATGTTGAGAGAG 985
Qy      261 IlePheArgAspGlnGlyIlyIlyAlaPhePheIlyGlyAla---Trp----- 275
Db      986 ATCTTCAGAGATGAGAGGCGCAAGGCTTCTTCAAGGGGTCAACACTGGAAACAAGGAGC 1045
Qy      276 ---SerAsnValIleuArgIlyMetGlyIlyAla 285
Db      1046 CTCGCGGAGCGCTCGAGGCTCACCTTCTGCA 1078

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RESULT 13
AAS91243
ID      AAS91243 standard; cDNA; 1156 BP.
XX      AAS91243;
DT      13-FEB-2002 (first entry)
DE      DNA encoding novel human diagnostic protein #27047.
XX      Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX      food supplement; medical imaging; diagnostic; genetic disorder; ss.
OS      Homo sapiens.

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XX      WO200175067-A2.
PN      11-OCT-2001.
XX      30-MAR-2001: 2001MO-US08631.
XX      31-MAR-2000: 2000US-0540217.
XX      23-AUG-2000: 2000US-0649167.
XX      (HYSE-) HYSEQ INC.
XX      Drmanac RT, Liu C, Tang YT;
XX      WPI: 2001-639362/73.
XX      P-PDB; ABG27056.
PT      New isolated polynucleotide and encoded polypeptides, useful in
PT      diagnostics, forensics, gene mapping, identification of mutations
PT      responsible for genetic disorders or other traits and to assess
PT      biodiversity.
PS      Claim 1: SEQ ID No 27047; 103pp: English.
CC      The invention relates to isolated polynucleotide (I) and
CC      polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC      polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC      and gene mapping, and in recombinant production of (II). The
CC      polynucleotides are also used in diagnostics as expressed sequence tags
CC      for identifying expressed genes. (I) is useful in gene therapy techniques
CC      to restore normal activity of (II) or to treat disease states involving
CC      (II). (II) is useful for generating antibodies against it, detecting or
CC      quantitating a polypeptide in tissue, as molecular weight markers and as
CC      a food supplement. (II) and its binding partners are useful in medical
CC      imaging of sites expressing (II). (I) and (II) are useful for treating
CC      disorders involving aberrant protein expression or biological activity.
CC      The polypeptide and polynucleotide sequences have applications in
CC      diagnostics, forensics, gene mapping, identification of mutations
CC      responsible for genetic disorders or other traits to assess biodiversity
CC      and to produce other types of data and products dependent on DNA and
CC      amino acid sequences. AAS64197-AAS94564 represent novel human
CC      diagnostic coding sequences of the invention.
CC      Note: The sequence data for this patent did not appear in the printed
CC      specification, but was obtained in electronic format directly from WIPO
CC      at ftp.wipo.int/pub/published_pct_sequences.
SQ      Sequence 1156 BP; 264 A; 286 C; 302 G; 303 T; 1 other;

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Alignment Scores:
Pred. No.: 1,81e-157 Length: 1156
Score: 1417.00 Matches: 274
Percent Similarity: 95.9% Conservative: 13
Best Local Similarity: 91.64% Mismatches: 9
Query Match: 91.83% Indels: 3
DB: 23 Gaps: 0

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US-09-811-094-33 (1-298) x AAS91243 (1-1156)
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Db      53  ATGACAGATGCCCTGTGCTCTTCCGCGCAAGACCTTCTTGCGAGTGGAGCGCGACCC 112
Qy      21  IleserlysthrAlaValAlaProIleGluArgValIlyLeuLeuGlnHis 40
Db      113  ATCTCCAGAGAGCGCGTGGCTCGATCGAGCGGCTCAACCTCTGTCGAGGTCGACGAT 172
Qy      41  AlaserlysglnIleAlaAlaAspIlysglnIleValAspCysIleValArg 60
Db      173  GCCAGCAGACAGATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 232
Qy      61  IleProlysglnGlnGlyValIleuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80
Db      233  ATTCGAGAGAGAGAGATCTGCTCTTCTGCGGCTGAACCTGGCAATGTCATTCACAGA 292

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Db 514 CTGGCTGGGAGCTGGGAGGATCTTCCAGCAGAAATTCATGGGCTGGGCGACTGT 573
 QY 161 leuValylsIlethrlYsSeraspGlyIleargGlyLeuTyrGlnGlyPheSerValSer 180
 Db 574 CTCACCAAGATCTTCAAGTCGAGCGCCGGAAGGCTCTTACAGAGGCTTTCAGTGTCTCT 633
 QY 181 ValGlnGlyIleIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaValGly 200
 Db 634 GTCCAGGCGCATCATATCATACAGAGCTGCTTCCGAGTCTATGACACCTGCGCAAGGGG 693
 QY 201 MetLeuProaspProLysasnThrHisIleValIleSerTrpMetIleAlaGlnThrVal 220
 Db 694 ATGCTGCCAGACCCCAAGAAATGTGCATATCTGAGCTGATGATTTCCCAAGATGTG 753
 QY 221 ThrAlaValAlaGlyValIleSerTyrProPheaspThrValArgTrgArgMetMet 240
 Db 754 ACAGCGCTGGCGGGCTGGTCTTATCCGTTGACACTGTTGCTGCTGAGATGATGATGANG 813
 QY 241 GlnSerGlyArgGlyValAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260
 Db 814 CAGTCTGGCCGCAAGGGGCTGATATATGTACACGGGACACTGACTGCTGGAGGAGG 873
 QY 261 IlePheArgaspGlyGlyGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuArg 280
 Db 874 ATTGCAAAAGATGAAGAGGACCAACGCTTCTTCAAAAGTGTGCTGCTCAATGACTGAGA 933
 QY 281 GlyMetGlyGlyAlaPheValIleuValLeuTyrAspGlyLeuLysValIle 298
 Db 934 GGCATGGGTGTGCTTTTGTATGTGATGATGATGATGATGATGATGATGATG 987
 RESULT 15
 AAV36480
 ID AAV36480 standard; DNA; 1259 BP.
 AC AAV36480;
 XX 28-SEP-1998 (first entry)
 DT
 XX
 DE Ant1 cDNA.
 XX
 XX Anti; Adenine nucleotide translocator; cloning; screening;
 KM DNA Tag diideoxy terminator cycle sequencing; oxidative phosphorylation;
 KM probe; OXPHOS; mitochondria; ADP; ATP; homozygous mutant; myopathy;
 KM hypertrophic cardiomyopathy; fascioscapular humeral muscular dystrophy;
 KM lactic acidosis; degenerative muscle disease; ss.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 190..1086
 FT /tag- a
 FT /product- "Anti protein"
 XX
 PN W09819714-A1.
 XX
 PD 14-MAY-1998.
 XX
 PE 31-OCT-1997; 97WO-US19882.
 XX
 PR 01-NOV-1996; 96US-0030017.
 XX
 PA (UYEM-) UNIV EMORY.
 XX
 XX Graham BC, Macgregor GR, Wallace DC;
 PI
 DR MPI; 1998-286608/25.
 XX
 XX Mice lacking heart-muscle adenine nucleotide translocator protein -
 PT useful as model for mitochondrial myopathy and hypertrophic
 PT cardiomyopathy in animals and to test therapeutic compositions or
 PT gene therapies
 XX
 PS Disclosure; Page 40; 61pp; English.

XX
 CC The present sequence is a mouse Anti degenerate cDNA sequence, cloned
 CC by screening a mouse heart cDNA library with the human Anti cDNA as a
 CC probe. The Anti cDNA sequence was determined by DNA Tag diideoxy
 CC terminator cycle sequencing. The Anti protein is encoded by the Anti
 CC locus, a nuclear gene on chromosome 8. This protein is required in
 CC mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP which
 CC can then be converted into ATP. An Anti homozygous mutant would thus be
 CC defective in OXPHOS which results in disease in oxidative metabolism
 CC dependent tissues. This mouse Anti homozygous mutant can be used as a
 CC model system for fascioscapular humeral muscular dystrophy, hypertrophic
 CC cardiomyopathy, myopathy, lactic acidosis, etc. These model systems can
 CC be used to test possible therapeutic compounds which increase/mediate ATP
 CC and ADP exchange across the mitochondrial membrane independent of ANT1.
 XX
 SQ Sequence 1259 BP; 274 A; 311 C; 339 G; 269 T; 66 other;
 Alignment Scores:
 Pred. No.: 5,35e-156 Length: 1259
 Score: 1405.00 Matches: 263
 Percent Similarity: 94.30% Conservative: 18
 Best Local Similarity: 88.26% Mismatches: 17
 Query Match: 91.06% Indels: 0
 DB: 19 Gaps: 0
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 QY 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyIleAlaAla 20
 Db 190 ATGGGGGATCAGGCTTGTAGCTTCTTAAAGACTTCTGCGAGTGGCATCGCGCGCC 249
 QY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
 Db 250 GTCTCCAGACGCGCGCTGCCGCCGATCGAGAGGCTCAAACTGCTGCGAGCTCCAGCAT 309
 QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
 Db 310 GCCAGCAACAGATCATGTCAGAGAGAGAGATCAAGGCACTCATGATTTGTGCGAGCA 359
 QY 61 IleProLysGluGlnIleValIleSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80
 Db 370 ATCCCAAGAGAGAGGCTTCTCTCTTCTTGAAGGGGTACCTGGCCAACTGATCCGG 429
 QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
 Db 430 TACTTCCCACTCAAGCCCTGAACCTTGCCTTCAAAAGACAAAGACAGACTTCTCCTG 489
 QY 101 GlyGlyValAlaAspLysHisThrGlnPheTrpArgTyrPheAlaLysLeuAlaSerGly 120
 Db 490 GGAGGGGTGATGCTAAGATAGAGTCTGCGCTTACTTCTGCTGAACCTGGGCTCTGGT 549
 QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
 Db 550 GGGGCGAGCTGGGCGCACTCCCTGCTGCTTACCCGCTGGACTTGTGTAGACACAGG 609
 QY 141 LeuAlaAlaAspValIleLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
 Db 610 CTGGCTGCCAGCTGGGCAAGGATGATCTCCACGAGAAATTCAAATGGGCTGGCGACTGT 659
 QY 161 LeuValLysIleIleIleIleTyrSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
 Db 670 CTCACCAAGATCTTCAAGTGGAGCGGCTGACGGGCTCTTACCAAGGCTTCAATGTCTCT 729
 QY 181 ValGlnGlyIleIleIleIleTyrArgAlaAlaTyrPheGlyValIleTyrAspThrAlaValGly 200
 Db 730 GTCCAGGCGATCATCATCTACAGAGCTGCTTACCTGGAGTCTATGACACTGCCAAGGGG 789
 QY 201 MetLeuProaspProLysasnThrHisIleValIleSerTrpMetIleAlaGlnThrVal 220
 Db 790 ATCTGCGCAGACCCCAAGAAATGTGCATATCTGAGCTGATGATGATGATGATGATG 849
 QY 221 ThrAlaValAlaGlyValIleSerTyrProPheaspThrValArgTrgArgMetMet 240

Thu Aug 28 08:34:55 2003

us-09-811-094-33.p2n.rng

Page 16

Db 850 ACAAGCGTGGCGGCTGCTCTTCCATCCGTTTGACACTGTTCGTAGATGATGATG 909
QY 241 GlnSerGlyArgGlySerGlyAlaAspIleMetTyrThrGlyValAspCysTyrArgLys 260
Db 910 CAGTCTGCCCCGCAAGGGCGCTGTAATTTATGTACACGGGCGACTGTGACTCTGAGAGAG 969
QY 261 IlePheArgAspGluGlyLysAlaPhePheLysGlyAlaTyrSerAsnValLeuArg 280
Db 970 ATTCGCAAAAGTGAAGAGCAACCGCTTCTTCAAAAGTGCTGTGCAATGTACTGAGA 1029
QY 281 GlyMetGlyLysAlaPheValLeuValLeuTyrAspGluLeuLysValIle 298
Db 1030 GGCAATGGGTGGTCTTTGTATTTGTAATGTATGATGATCAAAAAATATGTG 1083

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Job time : 343 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

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(without alignments)
3175.245 Million cell updates/sec

Title: US-09-811-094-33
Perfect score: 1543
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 22781392 segs, 12152238056 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09811094 -CGN.1.1.3549 -runat.26082003.110450.8053 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG.SCORES=0 -WAIT -DSPLOCK=100 -LONGIOG
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estipl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1543	100.0	1355	11	BC013256
2	1543	100.0	1355	11	BC013256
3	1543	100.0	1355	11	BC035469
4	1474	95.5	1201	13	BC019742
5	1463	94.8	1201	13	BC035361
6	1458	94.5	1201	9	AL545701
7	1454.5	94.3	1201	9	AL534908
8	1452.5	94.1	1071	12	BM554606
9	1451	94.0	949	13	BQ932832
10	1449	93.9	1201	9	AL540267
11	1445	93.6	1237	11	AK012751
12	1445	93.6	1239	11	AK003467
13	1440	93.3	1015	13	BC060934
14	1436	93.1	1185	9	AL515693
15	1434	92.9	1201	13	BC042493
16	1432	92.8	1201	13	BC039578
17	1431	92.7	1045	13	BC042095
18	1418	91.9	1201	9	AL557414
19	1418	91.9	1201	13	BC062646
20	1416	91.8	1201	9	AL539376
21	1414	91.6	1295	11	AK078077
22	1405	91.1	1014	13	BC037536
23	1404	91.0	1090	13	BC045752
24	1400	90.7	931	13	BQ933670
25	1400	90.7	1201	9	AL514420
26	1398	90.6	1119	13	BC015488
27	1396	90.5	1209	14	CD0496256
28	1393	90.3	1201	13	BC046463
29	1392	90.2	1236	11	AK002283
30	1390	90.1	999	13	BC0411074
31	1389	90.0	1146	14	CD0509246
32	1387	89.9	1030	12	BM476356
33	1385	89.8	1023	12	BM557479
34	1383	89.6	1201	13	BC0439582
35	1383	89.6	1528	11	BC050956
36	1382	89.6	922	13	BQ226117
37	1382	89.6	1142	14	CD050150
38	1380	89.4	931	12	B1409444
39	1380	89.4	1085	12	BM549432
40	1378	89.3	976	9	AL969048
41	1377.5	89.3	1055	13	BC015427
42	1377	89.2	1137	14	CD050238
43	1376	89.2	936	13	BQ512229
44	1375	89.1	939	13	BQ937030
45	1375	89.1	973	13	BC0447073

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS
BC013256	BC013256	1355 bp	mRNA	linear	HTC 27-AUG-2001				
BC013256	Homo sapiens, clone IMAGE:3865895, mRNA.								
BC013256	BC013256								
BC013256.1	GI:15501544								
HTC.	Homo sapiens (human)								
KEYWORDS	Homo sapiens								
ORGANISM	Homo sapiens								
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.								
AUTHORS	1 (bases 1 to 1355)								
	Strausberg, R.								

TITLE Direct Submission
JOURNAL Submitted (27-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgaps-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: villalona@bcm.tmc.edu, Villalón, D.K., Luna, R.A., Hale, S.M., Huiyik, S., Lu, X., Garcia, A.M., Holloway, M., Telford, B., Hodgson, A., Boucek, J., Yu, W., Muzny, D.M., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAX Plate: 13 Row: e Column: 10
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 3820534
This clone has the following problem: no 5' EST match.

FEATURES
source
Location/Qualifiers
1..1355
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3865895"
/tissue_type="Eye, retinoblastoma"
/clone_id="NIH_MGC_67"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"

BASE COUNT 283 a 417 c 404 g 251 t
ORIGIN

Alignment Scores:
Pred. NO: 4.09e-182 Length: 1355
Score: 1543.00 Matches: 298
Percent Similarity: 100.008 Conservative: 0
Best Local Similarity: 100.008 Mismatches: 0
Query Match: 100.008 Indels: 0
DB: 11 Gaps: 0

US-09-811-094-33 (1-298) x BC013256 (1-1355)

OY 1 MetTthGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAla 20
DB 92 ATACGGAAGAGGCGATCTCTTGGCCAAAGACTTCTTGGCGAGGAGCATGCCGCCGCC 151
OY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
DB 152 ATCTCCAAAGCGCGTGGCTGCATGAGCGGCTCAACCTCTCTCTCAAGTCCAGAC 211
OY 41 AlaserLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
DB 212 GCCAGCAACAGATGCGCGCGACAGCACTACAGGCGCATGCTGACTGATTCGCGC 271
OY 61 IleProLysGluGlnIleValLeuSerPheTyrArgGlyAsnLeuAlaAsnValIleArg 80
DB 272 ATCCCAAGAGGAGCGCGTGGCTCTCTCTGAGAGGGGCAACCTTGCCAAAGTATTCGC 331
OY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
DB 332 TACTTCCCACTCAAGCCCTCACTGCGCTTCAGAGATAGTACAGCAAGATCTTCTCG 391
OY 101 GlyGlyValAlaAspLysHisThrGlnPheTyrArgTyrPheAlaGlyAsnLeuAlaSerGly 120
DB 392 GGGGCGCTGACAGCAACAGCAAGTCTGTGAGAGTACTTGGCGGCAACCTGCCCTCCGCG 451

OY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
DB 452 GGTGCGCGCGGCGACATCTCTGTGTGTGTACCCGTGGATTCGCGCAAGACCCG 511
OY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
DB 512 CTGGCAGCGCGAGCTGGGAAAGTCAAGCAGACCGCGGAGATTCGAGGCTGGAGACTGG 571
OY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
DB 572 CTGCTGAAGATCAACCAAGTCCGAGCGCATCCGGGCGCTTACAGAGGCTTACGTGTC 631
OY 181 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
DB 632 GTGCAGGCGCATCATCTACCGGCGCGCTACTTGGCGGTGATACGATACGCGCAAGGCG 691
OY 201 MetLeuProAspProLysAsnThrHisIleValSerTyrMetIleAlaGlnThrVal 220
DB 692 ATGCTCCCGACCCCAAGACACACACATGCTGTGATGATGATCCGACACCGCTG 751
OY 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetLeuMet 240
DB 752 ACGGCGCTGGCGGCGGTGTGTCTACCCCTCGACACAGGTGCGGCGCGCATGATG 811
OY 241 GlnSerGlyArgLysGlyValAlaAspIleMetTyrThrGlyThrValAspCysTyrArgLys 260
DB 812 CAGTCCGCGCGCAAGAGACTGACATCATGTACACGCGCACCGTGCAGCTGTGGAGAG 871
OY 261 IlePheArgAspGluGlyLysValAlaPhePheLysGlyValAlaTyrSerAsnValLeuArg 280
DB 872 ATCTTCAAGATAGAGGCGGAGGCGCTTCTTCAAGGTGCGGTGCGCAAGTCTCGGG 931
OY 281 GlyMetClyGlyAlaPheValLeuValLeuTyrAspGluLeuLysIleValIle 298
DB 932 GGCATGGGCGCGCTTCTGCTGCTGTGACACAGCTCAAGAGGTATG 985

RESULT 2
BC035469 1355 bp mRNA linear HNC 31-JUL-2002
LOCUS
DEFINITION Homo sapiens, clone IMAGE:3867130, mRNA.
ACCESSION BC035469
VERSION BC035469.1 GI:22028373
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
DIRECT SUBMISSION
Submitted (31-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK
COMMENT
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgaps-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu, Villalón, D.K., Luna, R.A., Hale, S.M., Huiyik, S., Lu, X., Garcia, A.M., Holloway, M., Telford, B., Hodgson, A., Boucek, J., Yu, W., Muzny, D.M., Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAX Plate: 13 Row: f Column: 9
This clone was selected for full length sequencing because it

passed the following selection criteria: matched mRNA gi: 4503556
This clone has the following problem: no 5' EST match.

FEATURES

Location/Qualifiers
1..1355

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_image="3867130"
/tissue_type="Eye, retinoblastoma"
/clone_lib="NIR_MGC_67"
/lab_host="DH10B"
/note="vector: pCMV-SPOrt6"

BASE COUNT 283 a 417 c 404 g 251 t
ORIGIN

Alignment Scores:

Pred. No.:	4,09e-182	Length:	1355
Score:	1543.00	Matches:	288
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	11	Gaps:	0

US-09-811-094-33 (1-298) x BC035469 (1-1355)

```

QY      1 Metthrglunalaileserphealalyasphelualaglyglylealaala 20
DB      92 ATGACGGAACAGCCATCTCTCGCAAGACTTCTGGCGAGGCAATCGCGCGCC 151
QY      21 Ileserlythralavalaprollelgualgvalylsleuleuclnvalglnh 40
DB      152 ATCTCCAAAGCGCGGCGTCCGATCGAGCGGCTCAAGCTGCTGCGAGGCCGAC 211
QY      41 Alaserlysglnlealaalaspysglnlyrlysglylevalaspcysilevala 60
DB      212 GCCACCAACAGATCGCCGCCACAGCGATCGATCGATCGATCGATCGATCG 271
QY      61 Ileproulysglunlyvalleuserphertparglyasleualasavalilear 80
DB      272 ATCCCAAGAGGAGCGGCGTCTGCTCTGAGGCGCAACCTTCCCAAGCTATTCG 331
QY      81 Tyrrheprothrcinalaleuasnphelaphealyasplytyrlysglnleleu 100
DB      332 TACCTTCCCACTCAAGCCCTCAACTTCCCTTCAAGATAGATACAGAGATCTTC 391
QY      101 Glyglyvalaspyslethrcinphertparglyrphelaglyasleualaserg 120
DB      392 GGGGCGGTGACAGACAGCAGCTTCTGAGGATCTTGGCGCAACTGGCCCTCCG 451
QY      121 Glyalaalaglyalathserleucysphevaltyrproleuasphelaaargth 140
DB      452 GGTGGCGCGCGCGACCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 511
QY      141 Leualaalaasvalaglyysserglythrgluargglunphearglyleuglyap 160
DB      512 CTGGCAGCGGAGCTGGGAAGCTCAGCAGACAGCCGGAATTCGAGGCTGGAGAC 571
QY      161 LeuVallylelethrylseraspjlyleargglyleuTyrglnlypheserVal 180
DB      572 CTGGTGAAGATCAACCAAGTCCGACGAGCATCCGGGCGCTTACAGGCGCTTCA 631
QY      181 Valglnlylelelelethryrargalaalatyrrphelgylvaltyrasphthal 200
DB      632 GTGCAGGCGCATCATCTACCGGCGGCTACTTGGGCTGATGATAGAGCGCA 691
QY      201 MetleuproaspProlysasnthrsilevalasetrrmettlealaglnthral 220
DB      692 ATGCTCCCGACCCCAAGACAGCAGCATCTGCTGAGTGATGATCCGCGAGCCGT 751
QY      221 ThrAlaValAlaglyValalSerTyrrProphaspThValargargmetmet 240
DB      752 ACGGCGGTGGCGCGGTGCTCTTACCCCTTGCACAGCGGTGGCGGCGCATGATG 811

```

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QY      241 Glnserglyaluglyalaspillemetyrrthrglythvalaspysrrpargly 260
DB      812 CAGTCGGCGCGCAAGAGACTGACATCATCATGACAGCGGCGCATGCTGTGAGGA 871
QY      261 Ilepheargaspgluglyglylysalaphepelysglyalatrpsersnvallea 280
DB      872 ATCTTCAGAGATGAGGGGGCAAGCGCTTCTCAAGGTCGTCACACCTCCGCG 931
QY      281 GlymetglylvalaphelauvalleuTyrraspgluleuTyrsvalile 298
DB      932 GGCATGGGGGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 985

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RESULT 3
BX419742
LOCUS BX419742 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
DEFINITION BX419742 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
ACCESSION BX419742
VERSION BX419742.1 GI:30642547
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10389.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DF020B080P1&cluster=10389.r. Contact :
Feng Liang Email: fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID: CS0DF020B080P1.

FEATURES

Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DF020YCL6"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: Brain; Vector: pCMVSPORT_6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

BASE COUNT 245 a 365 c 354 g 210 t 27 others
ORIGIN

Alignment Scores:

Pred. No.:	1.51e-173	Length:	1201
Score:	1474.00 <td>Matches:</td> <td>292</td>	Matches:	292
Percent Similarity:	97.66% <td>Conservative:</td> <td>0</td>	Conservative:	0
Best Local Similarity:	97.66% <td>Mismatches:</td> <td>6</td>	Mismatches:	6
Query Match:	95.53% <td>Indels:</td> <td>2</td>	Indels:	2
DB:	13	Gaps:	0

US-09-811-094-33 (1-298) x BX419742 (1-1201)

```

QY      1 Metthrglunalaileserphealalyasphelualaglyglylealaala 20
DB      153 ATACGGAACAGCCATCTCTCGCAAGACTTCTGGCGAGGCAATCGCGCGCC 211
QY      21 Ileserlythralavalaprollelgualgvalylsleuleuclnvalglnh 40

```

Db 212 ATCTCCAGAGGCGCTGGCTCCGATCCAGGCGGCTCAAGCTGCTGCGAGTCCAGCAC 271
 QY 41 AAlaserlysglnllealaalaasplysglnlyrlysglyllevalaspccysllevalarg 60
 Db 272 GCCAGCAAGCAGATCCCGCCGACAGACAGTACAGAGGCGCTGCTGACGCTGCTGCTGCTG 331
 QY 61 Ileprolysglnllevalleuuserphterpargylasnualeuallaasvalilearg 80
 Db 332 ATCCCAAGAGCAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 391
 QY 81 Tyrphterparhrglnalleuasnphelaalaphelyasplysttyrlysglnllepheleu 100
 Db 392 TACTTCCCACTCAAGCCCTCAACTTCCCTTCAAGATTAAGTACAGACAGATCTTCTG 451
 QY 101 Glyglyvalasplyshsthrghlnphterpargyltyrphelaaglyasnualeualseerly 120
 Db 452 GGGGCGCGTGCACAGACAGACAGCTTCTGAGTACCTTGGGGCAACCTGGCGCTCGGC 511
 QY 121 Glylaalaglyalathrserleucysphterpargyltyrproleuaspphelaalargthary 140
 Db 512 GGTGGCGCGCGGAGMCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 571
 QY 141 leuallaalaasplyvalglylyserglythrghlnargluphterpargylleuaglyaspccys 160
 Db 572 CTGGCAGCGGACGTGGAGAAAGTCAAGGACAGAGCGCGAGTTCAGAGCGCTGGAGACATCC 631
 QY 161 leuvallysllethrlysserpargylleargglyleuarglynglynglypheserlyser 180
 Db 632 CTGGTGAAGATCACCAGTCCGACGACATCCGCGCGCGCGCGCGCTTCACTGCTGCTGCTG 691
 QY 181 valnglnlyllelellelethyrarglaalathrphelglyvaltyrparhtharalalyser 200
 Db 692 GTGGAGGCGATCATACATCTACCGGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 751
 QY 200 ymetleupproaspprolysanthrhllevallevalserthmetllealaglnthrya 220
 Db 752 CATGCTCCCGCCGACCAAGACAGACAGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 811
 QY 220 lthraalavalaalaglyvalasplyserlyrprophesparhtharalargargmetweme 240
 Db 812 GACGCGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 871
 QY 240 tglaserlysglyalaglyalaspillemetlyrthrghlythryalaspccyslyrparly 260
 Db 872 GCAGTCCGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 931
 QY 260 sllephetargasplynglylyslasphelphelysglyalatrpsersanvalleuar 280
 Db 932 GATCTTCACAGATGAGGGGGGCGAGGCTTCTTCAAGGGTGGCTGCTCAACGCTGCTGCG 991
 QY 280 gclymetglylyalaphelaaleuvalleuvaltyrparhtharalalyserlylle 298
 Db 992 GGGGATGGGGGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1046
 Db
 RESULT 4
 BK353661 1201 bp mRNA linear EST 05-MAY-2003
 LOCUS BK353661 Homo sapiens NEUROBLASTOMA COR 25-NORMALIZED Homo sapiens
 DEFINITION CDNA clone CS0DC0101K03 5'-PRIME, mRNA sequence.
 ACCESSION BK353661
 VERSION BK353661.1 GI:30375795
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1201)
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France

Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 11066.f. For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DC0101K03&cluster=11066.f. Contact:
 Feng Liang Email: fliang@life.com URL:
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID: CS0DC0101K02P1.
 Location/Qualifiers
 1..1201
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DC0101K03"
 /issue_type="NEUROBLASTOMA COR 25-NORMALIZED"
 /clone_id="Homo sapiens NEUROBLASTOMA COR 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 282 a 281 c 301 g 265 t
 ORIGIN

Alignment Scores:
 Pred. No.: 3, 6e-172 Length: 1201
 Score: 1463.00 Matches: 275
 Percent Similarity: 97.308 Conservative: 13
 Best Local Similarity: 92.918 Mismatches: 8
 Query Match: 94.828 Indels: 0
 DB: 13 Gaps: 0

US-09-811-094-33 (1-298) x BK353661 (1-1201)

QY 1 Methrglnllealaleserphterparhtharalalyserlyllealalealala 20
 Db 128 ATGACACATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 187
 QY 21 lleserlythrtharalavalaalaspillemetlyrthrghlythryalaspccyslyrparly 40
 Db 188 ATCTCCAGAGCAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 247
 QY 41 AAlaserlysglnllealaalaasplysglnlyrlysglyllevalaspccysllevalarg 60
 Db 248 GCACAGCAGCAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 307
 QY 61 lileprolysglnllevalleuuserphterpargylasnualeuallaasvalilearg 80
 Db 308 ATCCCAAGAGCGAGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 367
 QY 81 Tyrphterparhrglnalleuasnphelaalaphelyasplysttyrlysglnllepheleu 100
 Db 368 TACTTCCCACTCAAGCCCTCAACTTCCCTTCAAGATTAAGTACAGACAGATCTTCTG 427
 QY 101 Glyglyvalasplyshsthrghlnphterpargyltyrphelaaglyasnualeualseerly 120
 Db 428 GGTGGTGGGACAGAGAACCCGATTGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 487
 QY 121 Glylaalaglyalathrserleucysphterpargyltyrproleuaspphelaalargthary 140
 Db 488 GGTGGCGCGGCGAGACATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 547
 QY 141 leuallaalaasplyvalglylyserglythrghlnargluphterpargylleuaglyaspccys 160
 Db 548 CTAGCAGCGTGAATGGGTAAAGTGAAGTGAAGGAAATCCAGAGCCCTGGTGAATCC 607
 QY 161 leuvallysllethrlysserpargylleargglyleuarglynglynglypheserlyser 180
 Db 608 CTGGTGAAGATCTCAAAATCGATGAGGATTAAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 667
 QY 181 valnglnlyllelellelethyrarglaalathrphelglyvaltyrparhtharalalyser 200
 Db 668 GTGGAGGATTAATCATCTACAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 727

QY 201 MetleuproaspProlysaanthrhisllevalValSerTpmelllaaInthrVal 220
 DB 788 ATGCTTCGGATCCCAAGAACTCATCTGCATGATGATCCACAGACTGTC 787
 QY 221 ThrAlaValAlaGlyValValSerTyrProPheaspThrValArgArgmetMet 240
 DB 788 ACTGCTGTGCCGGGTGACTTCTATCCATTGACACCGTTCGCCGCGCATGATGATG 847
 QY 241 GlnSerGlyArgGlyGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260
 DB 848 CAGTAGGGCCGAAGAAGCACTGACATCATGACAGACGACCTTGCTGCGCGGAAG 907
 QY 261 IlePheArgAspGlyGlyGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuArg 280
 DB 908 ATTCGCTGATGAGAGGAGGCAACCTTTTTCAGGGGTCATGTCCTCAATGTCACGA 967
 QY 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLys 296
 DB 968 GGCATGGGTGTCTTTGTCTGCTGTGTGATGATGAATCAAGAG 1015

RESULT 5
 AL545701 1201 bp mRNA linear EST 31-MAY-2003
 LOCUS AL545701 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 DEFINITION clone CS0D1009YH03 5-PRIME, mRNA sequence.
 ACCESSION AL545701
 VERSION AL545701.2 GI:31267536
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1201)
 L1, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished
 On Feb 15, 2001 this sequence version replaced gi:12878183.
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr Web: www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 10389.r for
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0D1009CD020P1&cluster=10389.r. Contact :
 Feng Liang Email: fliang@life.techn.com/ Invitrogen Corporation 1600
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0D1009CD020P1.

FEATURES

source

1..1201
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D1009YH03"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."
 BASE COUNT 248 a 362 c 372 g 218 t 1 others
 ORIGIN

Alignment Scores:
 Pred. No.: 1,52e-171 Length: 1201
 Score: 1458.00 Matches: 290
 Percent Similarity: 97.32% Conservative: 1
 Best Local Similarity: 96.99% Mismatches: 6
 Query Match: 94.49% Indels: 3
 DB: 9 Gaps: 0

US-09-811-094-33 (1-298) x AL545701 (1-1201)

QY 2 ThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaIleAlaIle 21
 DB 51 TCCCGGATGCCATCTCCCTTCGGCAAGACTTCTTGCGGAGCGCAGCCTCCGCCGATC 110
 QY 22 SerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHisAla 41
 DB 111 TCCAGACGCGCGTGGCTCCGATCGAGCGGGTCAACCTCTGCTGACAGCTCCAGCAGCGCC 170
 QY 42 SerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArgIle 61
 DB 171 AGCAAGCAGATGCGCGCCGACAAAGCAAGGATGATGATGATGATGATGATGATGATGATG 230
 QY 62 ProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArgTyr 81
 DB 231 CCCAAGAGCAGAGCGCTGCTGCTCTTCTGAGGGGCAACCTTCCCAAGCTCATTCGCTTAC 290
 QY 82 PheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeuGly 101
 DB 291 TTCCCCACATCAAGCCCTCAACTTCGCTTCAAGGATGATGATGATGATGATGATGATGATG 350
 QY 102 GlyValAspLysHisThrGlnPheTrpArgTyrTrpPheAlaGlyAsnLeuAlaSerGlyGly 121
 DB 351 GCGGTGACAAAGCAGCAGCAGTTCGAGGTACTTTCGCGGCAACCTGCGCTCCGCGGT 410
 QY 122 AlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArgLeu 141
 DB 411 GCGCGCGCGCGCAACCTCCTCTGCTTCTGCTGATCCCTGATTTCCGCAAGCCCGCTG 470
 QY 142 AlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCysLeu 161
 DB 471 GCAGCGAGCTGGGGAAGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 530
 QY 162 ValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyLysHisSerValSerVal 181
 DB 531 GTGAATATCACCAAGTCCAGCGGATCCGCGGCTTACAGGCTTCAGTGTCTCCG 590
 QY 182 GlnGlyIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 201
 DB 591 CAGGATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 650
 QY 202 LeuProAspProLysAsnThrHisIleValAlaSerTyrPheMetIleAlaGlnThrValThr 221
 DB 651 CTCGCCGACCCCAAGAACAGCAGCATCGGTGATGATGATGATGATGATGATGATGATGATG 710
 QY 222 AlaValAlaGlyAlaValSerTyrProPheAspThrValArgArgmetMetGln 241
 DB 711 GCCGTGGCGCGCTGTGTCTTACCCCTTCGACAGCGTGGCGGCGCATGATGATGATGATG 770
 QY 242 SerGlyArgGlyGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLysIle 261
 DB 771 TCCGGGCGCAAGAGACTGACATCATGACAGCGCACGTC -CAGCTTGAGAGGAAGATC 829
 QY 262 PheArgAspGluGlyGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuArgGly 281
 DB 830 TTCAGAGATGAGGGGGGCAAGGCCCTTCAAGGGGCGCGGCGCAACGCTCGCGGGG 889
 QY 282 -MetLysGlyAlaPheValLeuValLeuTyrAspGluLeuLysLysValIle 298
 DB 890 CATGGGGGGCGCTTGT 942

RESULT 6
 AL534908 1201 bp mRNA linear EST 12-MAY-2003
 LOCUS AL534908 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
 DEFINITION CS0DF007YI20 5-PRIME, mRNA sequence.
 ACCESSION AL534908
 VERSION AL534908.2 GI:30541165
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

BASE COUNT 214 a 335 c 334 g 187 t 1 others
 ALIGNMENT SCORES:
 Pred. No.: 6,26e-171 Length: 1071
 Score: 1452.50 Matches: 292
 Percent Similarity: 97.34% Conservative: 1
 Best Local Similarity: 97.01% Mismatches: 3
 Query Match: 94.13% Indels: 5
 DB: 12 Gaps: 1

US-09-811-094-33 (1-298) x BM554606 (1-1071)

QY 1 MetThrGluGlnAlaIleSerPheAlaIleAspPheLeuAlaGlyIleAlaAla 20
 Db 13 ATGACGGAACAGGCGCATCTCTCGCCAAAGACTTCTGGCGAGGACATCGCGCGCC 72
 QY 21 IleSerIleThrAlaValAlaProIleGluArgValIleLeuLeuGlnValGlnHis 40
 Db 73 ATCTCCAGAGCGGCGCTGCTCCGATCGAGCGGGTCAGAGCTGCTGCTGCGAGTCCAGCAC 132
 QY 41 AlaSerIleGlnIleAlaAlaAspIleGlnIleValIleValAlaAspCysIleValArg 60
 Db 133 GCGAGCAGAGAGATCGCGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 192
 QY 61 IleProIleGluGlnIleValIleLeuSerPheTrpArgGlyAsnLeuAlaValIleArg 80
 Db 193 ATCCCAAG 252
 QY 81 TyrPheProThrIleAlaIleLeuAsnPheAlaPheIleAspIleValIlePheLeu 100
 Db 253 TACTTCCCACTCAACCGCTCAACCTTCTGCTTCAAGATTAAGTCAAGAGAGAGAGAGAGAG 312
 QY 101 GlyIleValAspIleValIleThrGlnPheTrpArgIlePheAlaGlnValAlaSerGly 120
 Db 313 GGGGGGCTGACAG 372
 QY 121 GlyAlaAlaGlyIleIleThrSerLeuCysPheValIleProLeuAspPheAlaArgThrArg 140
 Db 373 GGGGGGCGCGCGCGAGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 432
 QY 141 LeuAlaAlaAspValIleGlyIleValIleValIleValIleValIleValIleValIleVal 160
 Db 433 CTGGAGCGGAG 492
 QY 161 LeuValIleIleThrIleValIleSerAspGlyIleArgIleValIleValIleValIleVal 180
 Db 493 CTGGTGAAGATCAACCAAGTCCGAG 552
 QY 181 ValGlnGlyIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 200
 Db 553 GTCCAGGCGCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 612
 QY 201 MetLeuProAspProIleValIleValIleValIleValIleValIleValIleValIleVal 220
 Db 613 ATGCTCCCGAG 672
 QY 221 ThrAlaValAlaGlyValIleValIleValIleValIleValIleValIleValIleValIle 240
 Db 673 ACGGCGGTGGCGCGCGGTGGCGGTGGCGGTGGCGGTGGCGGTGGCGGTGGCGGTGGCGGTGGCG 732
 QY 241 GlnSerIleValIleValIleValIleValIleValIleValIleValIleValIleValIle 260
 Db 733 CAGTCCGCGCGAG 792
 QY 260 sIlePheArgAspGlnIleGlyIleValIleValIleValIleValIleValIleValIleVal 279
 Db 793 GATCTTCTAGAGATGAG 852
 QY 280 ArgGlyMetGlyIleValIleValIleValIleValIleValIleValIleValIleValIleVal 296
 Db 853 CGGGGGGAGATGGGGGGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 907

RESULT 8
 BQ932832
 LOCUS
 DEFINITION
 AGENCOURL_8824122 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:6459460
 ACCESSION
 BQ932832
 VERSION
 BQ932832.1
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens

REFERENCE
 1 (bases 1 to 949)
 NIH-MGC http://mhc.nci.nih.gov/
 TITLE
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL
 Unpublished
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: DCTD/DTF/gazdar
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: LNCM2644 row: j column: 05
 High quality sequence stop: 674.
 Location/Qualifiers
 1. 949
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6459460"
 /tissue_type="large cell carcinoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH-MGC_18"
 /note="Organ: lung; Vector: pOTB7; Site: 1; XhoI; Site: 2; EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCGAGGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MGC Library."

BASE COUNT 172 a 305 c 297 g 173 t 2 others
 ALIGNMENT SCORES:
 Pred. No.: 8.04e-171 Length: 949
 Score: 1451.00 Matches: 285
 Percent Similarity: 96.98% Conservative: 4
 Best Local Similarity: 95.64% Mismatches: 7
 Query Match: 94.04% Indels: 2
 DB: 13 Gaps: 0

US-09-811-094-33 (1-298) x BQ932832 (1-949)

QY 1 MetThrGluGlnAlaIleSerPheAlaIleAspPheLeuAlaGlyIleAlaAla 20
 Db 53 ATGACGGAACAGGCGCATCTCTCGCCAAAGACTTCTGGCGAGGACATCGCGCGCC 112
 QY 21 IleSerIleThrAlaValAlaProIleGluArgValIleLeuLeuGlnValGlnHis 40
 Db 113 ATCTCCAGAGAGCGGCGCTGCTCCGATCGAGCGGGTCAGAGCTGCTGCTGCTGCTGCTGCTG 172
 QY 41 AlaSerIleGlnIleAlaAlaAspIleGlnIleValIleValAlaAspCysIleValArg 60
 Db 173 GCGAGCAGAGAGATCGCGCGCGAG 232
 QY 61 IleProIleGluGlnIleValIleLeuSerPheTrpArgGlyAsnLeuAlaValIleArg 80
 Db 233 ATCCCAAG 292

Oy		81	TyrPheProThrGlnAlaLeuAspMetLysAspIleValSerGlyIlePheLeu	100
Db		293	TACTTCCCACTACAGCCCTCAACTTCCCTTCACAGATTAAGTACAAAGCATCTCTCCTG	352
Oy		101	GlyGlyValAspLysHisThrGlnPheTrpArgTyrrPheAlaGlyAsnLeuAlaSerGly	120
Oy		353	GGGGCGGGGACAGCACACAGAGTTCTGGAGGTACTTTGCGGGACAACCTGGCCCTCGGC	412
Oy		121	GlyAlaAlaGlyIleIleIleTyrArgAlaValIleTyrProLeuAspPheLysArgHyrArg	140
Db		413	GGTGCGGGCGGGGACCTCCCTCTGCTGCTGTTACCCTGGATTCTTCCGCAAGAACCCGC	472
Oy		141	LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys	160
Db		473	CTGGCAGCGGACCTGGGAAGTCAAGGCACAGAGCGCGATGCCAGGCTGGAGAGCTCC	532
Oy		161	LeuValLysIleIleTrpLysSerAspGlyIleArgGlyLeuTyrginglyPheSerValSer	180
Db		533	CTGGTAGAAGTACACCAAGTCCGACGAGCATCCGGGGCCCTGTACAGAGGCTTCAGTCTCC	592
Oy		181	ValGinglyIleIleIleIleTyrArgAlaAlaIleTyrPheGlyValTyrAspThrAlaLysGly	200
Db		593	GTCAGAGGAGTACATCATCTACCGGGCGGCTCTTCCGCGTACGATACGATAGGCCAAGGGC	652
Oy		201	MetLeuProAspProLysAsenThrHisIleValIleSerTTPMeIleAlaGlnThrVal	220
Db		653	ATGCTCCCGGACCCCAAGAACAGCACATCGTGGTACCTGAGATCGCGCAGACCGTG	712
Oy		221	ThrAlaValAlaGlyValIleSerTyrProPheAspThrValAlaArgAcGMeIleMet	240
Db		713	ACGGCCGTGGCGGGCTGTGTCTCTACCTTGACACAGCTGCGGGCGCAGATGATG	772
Oy		241	GlnSerGlyValTyrglyGlyAlaAspIleMetTyrThrGlyThrValAspCys-TTPArgTy	260
Db		773	CAGTCCGGGGCAAGAGAGCTGACATCATGTACACGGGACCGCTGCATGCTGTGGAGAA	832
Oy		260	glllePheArgAspGluGlyGlyValAlaPhePheTyrglyAlaTrpSerAsnValIleuar	280
Db		833	GATCTTCANAGATGAGGGGGGAGGCGCTTCTTCAAAGGTGGGTGTGCACGCTCTCGC	892
Oy		280	gGlyMetGlyGlyAla-PheValIleuValIleuTyrAspGluLeuLysValys	296
Db		893	GGGCATGGGGGGCGCCCTTCGTGCTGTCGATCAGAACTCAAGG	942
RESULT 9				
AL540267		1201 bp	mRNA	linear EST 31-MAY-2003
LOCUS	AL540267 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone			
DEFINITION	CSODF032YN01 5-PRIME, mRNA sequence.			
ACCESSION	AL540267			
VERSION	AL540267.2 GI:31264828			
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
REFERENCE	I.I.W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization			
AUTHORS	Unpublished			
TITLE	Contact: genoscope			
JOURNAL	Genoscope - Centre National de Sequencage			
COMMENT	BP 191 91006 Evry cedex - France Email: seqref@genoscope.cns.fr Web : www.genoscope.cns.fr was not normalized library was constructed by Life Technologies, division of Invitrogen. This sequence belongs to sequence cluster 10389.f for more information about this cluster, see http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq-CSODF032GC010PLICluster=10389.r. Contact : Reng Liang Email : filiang@lifetech.com URL : http://fulllength.invitrogen.com/ INVITROGEN Corporation 1600 Faraday Avenue Genoscope Sequence ID : CSODF032GC010PL.			

FEATURES
SOURCE

Location/Qualifiers
1. .1201

BASE COUNT
ORIGIN

349 C	331 g	210 C	20 C
-------	-------	-------	------

Alignment Scores:	
Pred. No.:	2, 04e-170
Score:	1449, .00
Percent Similarity:	98, 96%
Best local Similarity:	98, 96%
Best Match:	93, 91%
DB:	9
	Gaps:
	0
	1201
	286
	Matches:
	Conservative:
	0
	Mismatches:
	2
	Indels:
	3
	0
	Gaps:
	0

US-09-811-094-33 (1-298) x AL540267 (1-1201)

Oy	1	MetrhrGlnGlnAlaIleSerPheAlaIysAspPheLeuAlaGlyIleAlaAlaAla	20
Db	159	ATGAGCGAAGCGCATCTCTCCGCAAAACTCTTGCGCGAGATC-GCCGCCGC	217
Oy	21	IleSerIyStrAlaValAlaProIleGluArgValIysLeuLeuGlnValGlnHis	40
Db	218	ATCTCCAAAGCGCGCCGTGGCTCCGATCGAGGGGTCAACTCTCTCTGACGTCCAGAC	277
Oy	41	AlaSerIyGlnIleAlaAlaAspIyGlnIyIyGlyIleValAspCysIleValArg	60
Db	278	GCCAGACGACGATCGCCCGCGCAAGAGACAAAGGACGTGTGACTGTGATTCGCC	337
Oy	61	IleProIySGIuGInGlyValIleuSerPheTrpArgIyAsnLeuAlaAsnValIleArg	80
Db	338	ATCCCAAGAGACGAGCGCGTGTCTCTTCGAGGGGCAACCTTGGCCACGATATTCGC	397
Oy	81	TyrPheProTrGlnAlaIleuAsnPheAlaPheIyAspIyStrIyGlnIlePheIeu	100
Db	398	TACTTCCACACCAAGCCCTCACTTCGGCTTCAAGCATAGACAAACAGATTTCTG	457
Oy	101	GlyGlyValAspIyHisIleTrGlnPheTrpArgIyPheAlaGlyAsnLeuAlaSerGly	120
Db	458	GGGGGGGTGCACACACACGACGATTCGTGAGTACTTTCGGGGCAACCTGGCTTCGGGC	517
Oy	121	GlyAlaIleGlyAlaIleSerLeuCysPheValTyrProIeuAspPheAlaArgTrpArg	140
Db	518	GTTCGGCGCGGGGACCTCCCTCTCTCTGTCGATCCCGGTGGATTTCCCGCAAAACCGC	577
Oy	141	LeuAlaIleAspValGlyIySerGlyTrpGluArgGluPheArgIyLeuGlyAspCys	160
Db	578	CTGGCAGCGACGTGGGAAAGTACGAGACAGACCGCGAGTCCGAGCGCTGGAGACTGC	637
Oy	161	LeuValIyAlaIleThrIySerAspArgIyIleArgGlyLeuTyrGlnIyPheSerValSer	180
Db	638	CTGGTGAAGTCAACAAATCCGACGACATCCGGGGCTGTACACGGGGCTTCAGTGTCC	697
Oy	181	ValGlnGlyIleIleIleIyArgAlaAlaIyTrpPheGlyValTyrAspTrhAlaIyGly	200
Db	698	GTGAGAGGCACTACTCTACCGGGGGCGCTTACTTCGGCGTGTACGATACGGCCAAAGGC	757
Oy	201	MetLeuProAspProIyAsnTrhHisIleValAlaSerTrpMetIleAlaGlnTrhVal	220
Db	758	ATGCTCCCGACCCCAAGACACGACATCTGTGTACTGTGAATGATCGCGCAACCTTG	817
Oy	221	ThrAlaValAlaGlyAlaValSerTyrProIleAspTrhValArgArgGlyMetMet	240

Db	818	ACGGCGTGGCCGCGTGATGTCTACCCTTCAGACACGGTGC GGCGGCGCATGATGANTG	877
Oy	241	GInsercIyArtydYsgIyAlaAspIlleMeTyrrThrclyThrValaSpCySTrPaRylus	260
Db	878	CAGTCCCGGGGCCAAGAAGAGCTGACATCATGTACACGGGGCACGTCCGACTGTGGAGGAAG	937
Oy	261	IlePhetrYgaSpJugIysYgLyLysAlaPhePhetYsgIyAlaTrpsSerAanValLeuaRg	280
Db	938	ATTCTCAGAGNTGAGGGGGGGCCAAAGCCCTTTCTTCAAGSGTGCTGTGTCACACGTCTCGGG	997
Oy	281	GIyMetcIyglYalaphaeValleuaI 289	
Db	998	GGCATGGGGGGSSGC-TTCGTGCTCTGTC 1023	
RESULT 10			
LOCUS	AK012751		
DEFINITION	AK012751	1237 bp mRNA linear HTC 05-DEC-2002	
ACCESSION	AK012751	Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length	
VERSION	AK012751.1	enriched library, clone:2810016M9 product:solute carrier family 25	
KEYWORDS	HTC; CAP trapper.	(mitochondrial carrier; adenine nucleotide translocator), member 5,	
SOURCE	Mus musculus (house mouse)	full insert sequence.	
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.		
TITLE	Carninci, P. and Hayashizaki, Y.		
JOURNAL	High-efficiency full-length cDNA cloning		
MEDLINE	Meth. Enzymol. 303, 19-44 (1999)		
PUBMED	99279253		
REFERENCE	10349636		
AUTHORS	2		
TITLE	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,		
JOURNAL	Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
MEDLINE	Normalization and subtraction of cap-trapper-selected cDNAs to		
PUBMED	prepare full-length cDNA libraries for rapid discovery of new genes		
REFERENCE	Genome Res. 10 (10), 1617-1630 (2000)		
AUTHORS	3		
TITLE	Shibata, K., Itoh, M., Alzawa, K., Nagao, S., Sasaki, N., Carninci, P.,		
JOURNAL	Kono, H., Akiyama, D., Nishi, K., Kitsumori, T., Tashiro, H., Itoh, M.,		
MEDLINE	Sunji, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,		
PUBMED	Yamanoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasaiyagi, K.,		
REFERENCE	Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,		
AUTHORS	Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,		
TITLE	Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.		
JOURNAL	RIKEN integrated sequence analysis (RISA) system--384-format		
MEDLINE	sequencing pipeline with 384 multicapillary sequencer		
PUBMED	Genome Res. 10 (11), 1757-1771 (2000)		
REFERENCE	4		
AUTHORS	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,		
TITLE	Arikawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, J., Fukuda, S.,		
JOURNAL	Alzawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, K.,		
MEDLINE	Salto, T., Okazaki, Y., Gotohori, T., Bono, H., Kasukawa, T., Salto, R.,		
PUBMED	Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,		
REFERENCE	Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochwa, H.,		
AUTHORS	Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G.,		
TITLE	Quackenbush, J., Schriml, L.M., Stamboli, F., Suzuki, R., Tomita, M.,		
JOURNAL	Wagner, L., Mashio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,		
MEDLINE	Baldarelli, R., Barsh, G., Blake, J., Bozell, D., Bojunga, N.,		
PUBMED	Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bull, C.,		
REFERENCE	Etcherich, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,		
AUTHORS	Hochmann, L., Hume, D.A., Kamlya, M., Lee, N.H., Lyons, P.,		
TITLE	Matsumoni, L., Mashima, J., Mazzarella, J., Momhaerts, P.,		
JOURNAL	Ring, B., Ringwald, C., Seya, T., Shibata, Y., Storck, K.F., Suzuki, H.,		
MEDLINE	Sato, K., Schonbach, C., Seta, T., Shibata, Y., Storck, K.F., Suzuki, H.,		
PUBMED	Sato, K., Wang, K.H., Weltz, C., Whittaker, C., Wilming, L.,		
REFERENCE	Toyo-Oka, K., Wang, K.H., Weltz, C., Whittaker, C., Wilming, L.,		

TITLE	Yoshinawa-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohsaki,S.
JOURNAL	and Hayashizaki,Y.
MEDLINE	Functional annotation of a full-length mouse cDNA collection
PUBMED	Nature 409 (6821), 685-690 (2001)
REFERENCE	21085660
AUTHORS	11217851
TITLE	5 The FANTOM Consortium and the RIKEN Genome Exploration Research
JOURNAL	Group Phase I & II Team.
REFERENCE	Analysis of the mouse transcriptome based on functional annotation
AUTHORS	of 60,770 full-length cDNAs
	Nature 420, 563-573 (2002)
	6 (bases 1 to 1237)
	Aachari,U., Alizadeh,K., Akahira,S., Akimura,T., Arai,A., Aono,H.,
	Arakawa,T., Bono,H., Carlinici,P., Fukuda,S., Fukushima,Y.,
	Furuno,M., Hanagaki,T., Harai,A., Hayatsu,N., Hiramoto,K.,
	Hirooka,T., Horii,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M.,
	Kasukawa,T., Kato,H., Kawai,J., Koike,Y., Konno,H., Kouda,M.,
	Koyama,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishikawa,K.,
	Nomura,K., Numasaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C.,
	Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Saeki,K.,
	Shibata,K., Shibata,Y., Shingawa,A., Shiraki,T., Sogabe,Y.,
	Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T.,
	Tajima,Y., Toyota,T., Yamamura,T., Yasunishi,A., Yoshida,K.,
	Yoshino,M., Yumatsugu,M. and Hayashizaki,Y.
TITLE	Direct Submissions
JOURNAL	Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
	Physical and Chemical Research (RIKEN), Laboratory for Genome
	Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
	RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama,
	Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
	URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
	Fax:81-45-503-9216)
COMMENT	Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
	cDNA library was prepared and sequenced in Mouse Genome
	Encyclopedia Project of Genome Exploration Research Group in Riken
	Genomic Sciences Center and Genome Science Laboratory in RIKEN.
	Division of Experimental Animal Research in Riken contributed to
	prepare mouse tissues. First strand cDNA was primed with a primer
	[5' GAGACGAAGAAGATCCAAAGCCTCTTTTCTTTTCTTTTNN 3'], cDNA was
	prepared by using trehalose thermo-activated reverse transcriptase
	and subsequently enriched for full-length by cap-trapper. cDNA went
	through one round of normalization to Rot = 7.5 and subtraction to
	Rot = 37.5. Second strand cDNA was prepared with the primer adapter
	of sequence [5'
	GAGAGGAGATCTCTCGAGTTAATTAAATAATCCCCCCCCCCC 3']. cDNA was cleaved
	with XhoI and SctI. Cloning sites, 5' end: XhoI; 3' end: SctI.
	Host: SOLR.
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	/clone="2810016M09"
	/tissue_type="whole body"
	/clone_lib="RIKEN full-length enriched mouse cDNA library"
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	LVTXKSDWRTKGLGYGVNVSVQGITLIIRAAYFGIYDPARKMLPDPKNTHTFIEMWIAQ

TITLE	Group Phase I & II Team.
JOURNAL	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
REFERENCE	Nature 420, 563-573 (2002)
AUTHORS	6 (bases 1 to 1337)
	Adachi,J., Aizawa,K., Akimura,T., Atakawa,T., Bono,H., Carninci,P.

TITLE	JOURNAL REFERENCE	AUTHORS
Group Phase I & II team. Analysis of the transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)	6 (bases 1 to 1237)	Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Futuno,M., Hanagaki,T., Hara,A., Hashizume,M., Hayashida,K., Hayatsu,N., Hirotsu,K., Hirooka,T., Hirozane,T., Horii,F., Imotohi,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Kato,H., Kawaji,T., Kohjima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishikawa,K., Nomura,K., Numasaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeba,Y., Tanaka,T., Tomaru,A., Toyota,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
Direct Submission Submitted (16-Apr-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suheiho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome.res@gsr.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)	CNDA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge. Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/ URL:http://fantom.gsc.riken.go.jp/. Location/Qualifiers	1. 1237 /organism="Mus musculus" /mol_type="mRNA" /strain="NOD" /db_xref="PANTOM.DB:E430024K03" /db_xref="taxon:10090" /clone="E430024K03" /cell_type="thymic cells" /tissue_type="thymus" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="2 days neonate" 78..974 /note="unnamed protein product; putative soluble carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 (MDJMG1.135496)" /codon_start=1 /protein_id="BAC40533.1" /db_xref="GI:26353806" /translation="MTDAVSPAFKDFLAGVAAIASTAVAPIERVKLLLOVOHASKQITADAKYIICDVAIRPEKGVLSFMGNLANVIRPTALNFADCKIQIFLGVRKIDRFMYRFGANLASGAAGATSCIEFYADFARTLADVGAEREKFGIGDC LKIVYSDDIKGLIOGFNSVGGIIYAAYGYIDTKMKPPDKNRTFTSMWINS VTAVALGLTSFPDYRRMMMQSGRKGDIMYTCTILDCWKRIADESKAFPGAMS NVLRKGGAFLVLIDEIKKY"
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polyA_site	1237	
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ORIGIN	/note="putative"	
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Pred. No.:	1445 00 Matches: 271	
Score:	96.628 Conservative: 15	

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 QY 11eProlysglulnglnlyalleuserphetrpargylasneualasnailllearg 80
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 QY 121 GlyAlaAlaGlyAlaThrserleucysphevaltyrProleuaspphealargthrarg 140
 DB 441 GGTGGCGGTGGGCTCATCTGCTGCTTGTGTACCTCTTATTTTGGCCGTACCCGT 500
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 QY 161 leuVallyllethrlysseraspglylleargglyleuylrlynglypheaserValser 180
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 QY 261 llepheargaspcluglylyllyslalaaphepelysglyalatrpsersnaValleuarg 280
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 QY 281 GlyMetGlyGlyAlaPheValleuValleuTyrAspGluLeuLyslys 296
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 ACCESSION BX360934
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 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 1015)
 AUTHORS Li, W.-B., Gruber, C., Jessee, J., and Polyes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 11066.f For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0D1077CA090P1&cluster=11066.f. Contact :
 Feng Liang Email : fliang@life.techn.com url :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
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 ORIGIN
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 DB 308 ATTCCAAGGAGAGGAGGATGCTGCTTCTGCGCGGTAACTGGCCAATGTCATCAGA 367
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VERSION	BX424943.1		
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 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 1201)
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr Web: www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 11066.f for
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CL0BA004ZF03RPLcluster=11066.f. Contact :
 Peng Liang Email: filiang@life.techn.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CL0BA004ZF03RPL.

FEATURES
 source
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 the Not I and EcoRV sites of the pCMVSPORT 6 vector.
 Library was not normalized."
 BASE COUNT 268 a 272 c 306 g 318 t 37 others
 ORIGIN

Alignment Scores:
 Pred. No.: 1.5e-168 Length: 1201
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 Best Local Similarity: 91.53% Mismatches: 12
 Query Match: 92.94% Indels: 0
 DB: 13 Gaps: 0

US-09-811-094-33 (1-298) x BX424943 (1-1201)

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 Db 131 ATGACAGATGCCGCTGTCTTCGCCAAGACTTCTCGCAGGTGCGCGCCGCC 190

QY 21 IleSerLySThrAlaValAlaProIleGluArgValIysLeuLeuGlnValGlnHis 40
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QY 41 AlaSerLyGlnIleAlaAlaAspLyGlnIleValAlaAspCysIleValArg 60
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QY 181 ValGlnGlyIleIleLeuTyrArgAlaAlaTyrPheGlyValTyrAspPheAlaValGly 200
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 Db 671 GTGCAAGGATTAATCATCTACCGAGCGCTTCTGTGATCATGACACTGCAAGGGA 730

QY 201 MetLeuProAspProLyAsnThrHisIleValAlaSerTrpMetIleAlaGlnThrVal 220
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 Db 731 ATGCTCCGAGATCCCAAGAACACTCATCTCATCATGAGTGTATGTCACAGACTGTY 790

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 Db 851 CAGTTAGGCGGCAAGGAACCTGACATCATGATACAGGACAGCTTGAATGTCGCGGAAG 910

QY 261 IlePheArgAspGluGlyLyIysAlaPhePheLyGlyAlaTrpSerAsnValLeuArg 280
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 Db 911 ATTGCTCGATGAAGAGGCAAGAGCTTTTTCAGAGGTGATGATGCAATGTTCTCACA 970

QY 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLys 295
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 Db 971 GGCATGGGTGTGCTTTGTGCTTCTTGTATKATGAAMWYAGA 1015

Search completed: August 27, 2003, 14:22:16
 Job time : 2291 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: August 27, 2003, 11:59:10 ; Search time 86 Seconds

(without alignments)
1529,444 Million cell updates/sec

Title: US-09-811-094-33

Perfect score: 1543
Sequence: 1 MTQQAISFAKDFLAGIAAA.....LRGNGAFVLYLDELKRV1 298

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=Issued_Patents_NA -OPMT=fastat -SUFFIX=p2n.rni -MIMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=Dlcs -START=1 -END=1 -MATRIX=dlcosum62 -TRANS=human40.cdl
-LIST=45 -DOCALLIGN=200 -THR.SCORE=pcr -THR.MAX=100 -THR.MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09811094.8CGN.1.1.103.8runat.26082003.110451.8070 -NCPU=6 -ICPU=3
-NO_MMAP -LARGESOURCY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -Ygapop=10 -Ygapext=0.5 -Delop=6 -Delext=7

Database :

Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A.COMB.seq:*
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5: /cgn2_6/ptodata/2/ina/PCYUS.COMB.seq:*
6: /cgn2_6/ptodata/2/ina/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1543	100.0	897	4	US-09-434-354-3 Sequence 3, Appl1
2	1543	100.0	1212	4	US-09-620-312D-687 Sequence 687, App
3	1454	94.2	897	4	US-09-434-354-2 Sequence 2, Appl1
4	1412	91.5	1177	3	US-08-961-871-9 Sequence 9, Appl1
5	1405	91.1	1259	3	US-08-961-871-11 Sequence 11, Appl1
6	1385.5	89.8	894	4	US-09-434-354-1 Sequence 1, Appl1
7	314	20.3	3334	4	US-09-996-243-288 Sequence 288, App
8	311	20.2	1816	3	US-09-188-930-262 Sequence 262, App
9	311	20.2	1816	4	US-09-312-283C-262 Sequence 283, App
10	299.5	19.4	2663	4	US-09-620-312D-283 Sequence 622, App
11	294	19.1	289	4	US-09-016-434-622 Sequence 26, Appl
12	286	18.5	1674	4	US-09-482-273-26

13	283.5	18.4	876	4	US-09-501-558-1	Sequence 1, Appl1
14	280	18.1	1443	4	US-09-160-119-3	Sequence 3, Appl1
15	280	18.1	2095	4	US-09-160-119-1	Sequence 1, Appl1
16	265	17.2	1192	3	US-09-142-565-1	Sequence 1, Appl1
17	250.5	16.2	1255	1	US-08-518-878B-38	Sequence 38, Appl1
18	250.5	16.2	1255	1	US-08-294-522B-38	Sequence 38, Appl1
19	250.5	16.2	1255	2	US-08-470-868A-38	Sequence 38, Appl1
20	250.5	16.2	1255	2	US-08-807-861A-38	Sequence 38, Appl1
21	250.5	16.2	1596	3	US-09-210-681-38	Sequence 38, Appl1
22	250.5	16.2	1596	3	US-08-946-719A-38	Sequence 38, Appl1
23	250.5	16.2	1596	4	US-09-547-983-38	Sequence 38, Appl1
24	245	15.9	1949	2	US-08-937-466-3	Sequence 3, Appl1
25	245	15.9	1949	2	US-09-172-528-3	Sequence 3, Appl1
26	245	15.9	1949	3	US-09-318-199-3	Sequence 3, Appl1
27	245	15.9	1949	3	US-09-503-579-3	Sequence 3, Appl1
28	244	15.8	2782	2	US-08-937-466-1	Sequence 1, Appl1
29	244	15.8	2782	2	US-09-172-528-1	Sequence 1, Appl1
30	244	15.8	2782	3	US-09-318-199-1	Sequence 1, Appl1
31	244	15.8	2782	3	US-09-503-579-1	Sequence 1, Appl1
32	239.5	15.5	1764	4	US-09-620-312D-548	Sequence 548, App
33	233.5	15.1	1594	2	US-08-933-750C-61	Sequence 61, App
34	233.5	15.1	1594	3	US-09-234-613-61	Sequence 61, App
35	230	14.9	1679	4	US-09-620-312D-997	Sequence 997, App
36	228.5	14.9	1566	4	US-09-620-312D-63	Sequence 63, App
37	227.5	14.7	1205	1	US-08-518-878B-36	Sequence 36, App
38	227.5	14.7	1205	1	US-08-294-522B-37	Sequence 37, App
39	227.5	14.7	1205	2	US-08-807-861A-36	Sequence 36, App
40	227.5	14.7	1205	2	US-08-470-868A-36	Sequence 36, App
41	227.5	14.7	1205	3	US-09-210-681-36	Sequence 36, App
42	227.5	14.7	1205	3	US-08-946-719A-36	Sequence 36, App
43	227.5	14.7	1205	4	US-09-547-983-36	Sequence 36, App
44	222	14.4	882	4	US-09-501-558-3	Sequence 3, Appl1
45	214	13.9	1341	4	US-09-620-312D-207	Sequence 207, App

ALIGNMENTS

RESULT 1
US-09-434-354-3
; Sequence 3, Application US/09434354
; Patent No. 6562563
; GENERAL INFORMATION:
; APPLICANT: Murphy, Anne N.
; APPLICANT: Cleveneger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Andreyev, Alexander Y.
; APPLICANT: Frigel, Luciano G.
; APPLICANT: Vellelebl, Gonul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
; TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
; FILE REFERENCE: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS
; CURRENT APPLICATION NUMBER: US/09/434,354
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 897
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-434-354-3
Alignment Scores:
Pred. No.: 9.07e-180
Score: 1543.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 4
Gaps: 0
Matches: 897
Conservative: 298
Mismatches: 0
Indels: 0

US-09-811-094-33 (1-298) x US-09-434-354-3 (1-897)

[illegible]

US-09-620-312D-687
 : Sequence 687, Application US/09620312D
 : Patient NO. 65696652
 :
 : GENERAL INFORMATION:
 : APPLICANT: Tang, Y. Tom
 : APPLICANT: Liu, Chenghua
 : APPLICANT: Asundi, Vinod
 : APPLICANT: Zhang, Jie
 : APPLICANT: Ren, Feiyun
 : APPLICANT: Chen, Rui-hong
 : APPLICANT: Zhao, Qing A.
 : APPLICANT: Wehrman, Tom

APPLICANT: Xue, Aiding J.
 APPLICANT: Yang, Yonghong
 APPLICANT: Wang, Jian-Pui
 APPLICANT: Zhou, Ping
 APPLICANT: Ma, Yundong
 APPLICANT: Wang, Dunrui
 APPLICANT: Wang, Zhiwei
 APPLICANT: John Tillimphast
 APPLICANT: Dimaac, Radoles T.
 TITLE OF INVENTION: NO. 6556962e1 Nucleic Acids and
 TITLE OF INVENTION: Polypeptides
 FILE REFERENCE: 784CIP2B
 CURRENT APPLICATION NUMBER: US/09/620,312D
 CURRENT FILING DATE: 2000-07-19
 PRIOR APPLICATION NUMBER: 09/552,317
 PRIOR FILING DATE: 2000-04-25
 PRIOR APPLICATION NUMBER: 09/488,725
 PRIOR FILING DATE: 2000-01-21
 NUMBER OF SEQ ID NOS: 1105
 SOFTWARE: pl_FL-genes Version 1.0
 SEQ ID NO 687
 LENGTH: 1212
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (131)..(1027)
 US-09-620-312D-687

Alignment Scores:	1.42e-179	121
Pred. No.:	1543	298
Score:	100.00%	
Percent Similarity:	100.00%	
Best Local Similarity:	100.00%	
Query Match:	4	
DB:	100	
	Gaps:	0

US-09-811-094-33 (1-298) x US-09-620-312D-687 (1-1212)

Oy	1	Metntrnglgnlala1lleserPhealalyasphleu1aagly1l1a1a1a1a1a	20
Db	131	ATGAGGAAACAGGGCAACTCTTCCTGGCAAAACATCTTGGCCGAGAGCATGGCCGGCC	190
Oy	21	l1eserLystrAlaValAlaPro1l1eg1uarValLysLeu1euleug1nvalGlnHis	40
Db	191	ATCTCCAAAGCGCCGTCGGCTCGATCGAGCGGGGTCAAGCTGTGCTGCAGTCCACAC	250
Oy	41	AlaSerLySGln1leAla1a1aap1ySGln1rLySG1y1leValaSPcys1leValArg	60
Db	251	GCACGACAGCAAGATCGCGCGCGACAGCATGTCACAAGGCACTCTGACATCGCATGGTCC	310
Oy	61	l1aProLySGln1ng1yVal1leuSerPhe1rPArg1yAsn1eula1aAsnVal1leArg	80
Db	311	ATCCCCAAGACAGAGGGCGTCTGCTCTTCGTGAGGGGCAACTTCCCAAGCATATTCG	370
Oy	81	TyrPheProthGln1Ala1euaAsn1PheAla1PheLySaSP1yTrLySGln1lePhe1eu	100
Db	371	TACTCCCACTCAAGCCCTTCACTTCGCTTCAGAGTAAGTACAAAGCAGATCTTCTCG	430
Oy	101	G1yG1yValaSP1yHis1rthGlnPhe1rPArg1yTrPhe1aG1yAsn1eula1aSerG1y	120
Db	431	GGGGGGGTGAACACACACGCAAGTCTGGAAGTACTTTGGCGGCAACTGGCCCTCGGGC	490
Oy	121	G1yAla1aG1yAla1rSer1eucySPheVal1yPro1euaSPheAla1rGh1Arg	140
Db	491	GGTCCGGCGGGCGCACCTCCCTCTGTCTGCTTCACCCGCTGGCATTTTCGCAAAACCCG	550
Oy	141	Leu1a1a1aSPVal1G1yLySerG1yTrthG1uaG1uPheArg1yLeuG1yAspCys	160
Db	551	CTGGCAGCGGAGGTGGGAAATCAGGACAGAGCCCGAGTTCACAGCCCTGGGAACATGC	610
Oy	161	LeuVal1yS1lethLySerASP1y1leArg1yLeu1yTrGln1yPheSerVal1Ser	180

Db 611 CTGGTGAAGATCCAGCATCCGAGCGCATCCGGGCTGTACACAGGCTTCAAGTGTCTCC 670
QY 181 ValGInGlyIleIleIleTyrAlaAlaIleTyrPheGlyValTyrAspThrAlaIleGly 200
Db 671 GTGAGGGGATCATCATCTACCGGGGCTTCTTCCGGGGTGTACATACGGCCAAAGGC 730
QY 201 MetLeuProAspProLysAsnThrHisIleValIleSerTrpMetIleAlaGlnThrVal 220
Db 731 ATGCTCCCGGACCCGACACGACATCGGTGACGTGATCATCGCCGACGACCGGTG 790
QY 221 ThrAlaValAlaGlyValIleValSerTyrProPheAspThrValArgArgMetMet 240
Db 791 ACGGCGGTGGCCGGGCTGTGTCTTCCATCCCTTCGACGCGGTGCGCGGCGCATGATGAG 850
QY 241 GlnSerGlyArgGlyValAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260
Db 851 CAGTCCGGGGCGAAAGAGGCTGACATCATGTACAGGGGACCGTGCAGCTGTGGAGAG 910
QY 261 IlePheArgAspGluGlyGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuArg 280
Db 911 ATCTTCAGAGATGAGAGGGGGGCGAAGGCTTCTTCAAGGGGTGCGTCCAACTCTCGCG 970
QY 281 GlyMetGlyGlyAlaPheValIleuValIleuTyrAspGluLeuLysValIle 298
Db 971 GGCATGGGGGGCGCTTGTGTGTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1024

RESULT 3

US-09-434-354-2
; Sequence 2, Application US/09434354
; Patent No. 6562563
; GENERAL INFORMATION:
; APPLICANT: Murphy, Anne N.
; APPLICANT: Clewenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Andreyev, Alexander Y.
; APPLICANT: Frigieri, Luciano G.
; APPLICANT: Vellicelebi, Gonul
; APPLICANT: Davis, Robert E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
; TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
; TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS
; FILE REFERENCE: 660088.433
; CURRENT APPLICATION NUMBER: US/09/434,354
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 897
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-434-354-2

Alignment Scores:

Pred. No.: 7,39e-169 Length: 897
Score: 1454.00 Matches: 274
Percent Similarity: 96.96% Conservative: 13
Best Local Similarity: 92.57% Mismatches: 9
Query Match: 94.23% Indels: 0
DB: 4 Gaps: 0

US-09-811-094-33 (1-298) x US-09-434-354-2 (1-897)

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Db 1 ATGACAGATGCGCATTTGCTTCGCAAGAGACTTCTGTGCGAGTGTGAGTGTGCGCGAGCC 60
QY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuLeuGlnValGlnHis 40
Db 61 ATCTCCAGAGACGCGGTGACCGCCATCGAGCGGTCACAGCTGCTGTGACGAGTGCAGCAT 120
QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAlaPspCysIleValArg 60
Db 121 GCCACGACAGACATCTCTCCAGATTAAGCATACAAAGGCAATTATGACTGCGGTGCGGT 180

QY 61 IleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80
Db 181 ATTCACAGAGACAGAGAACTCTGTCTTCTGCGGGATTAACCTGGCCAAATCATCA 240
QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
Db 241 TACTTCCCGACCCAGGCTCTTAACTTCGCTTCAAGATTAATACAAAGACGATCTTCCG 300
QY 101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120
Db 301 GGTGTGTGACAGAGAGAACCCAGTTTGTGCGCTTACTTGTGACAGGATTTGGCATCGGT 360
QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
Db 361 GGTGGCGGAGGGGCGACATCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlnLysPys 160
Db 421 CTAGCAGCTGATGTGGTAAAGCTGAGCTGAAGGGAATTCGAGGCTCGGTGACTGC 480
QY 161 LeuValIleValIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
Db 481 CTGGTTAAGATCTCAAAATCTGATGAGATTAAGGCTGTATCCAAAGCTTTAACTGTCT 540
QY 181 ValGInGlyIleIleIleTyrAlaAlaIleTyrPheGlyValTyrAspThrAlaIleGly 200
Db 541 GTGACAGGATATATATCATCTACAGAGCGGCTTCTGATCATATACATGCAAGGA 600
QY 201 MetLeuProAspProLysAsnThrHisIleValIleSerTrpMetIleAlaGlnThrVal 220
Db 601 ATGCTTCGCGATCCCAAGAACACTCACATCGCATCGATGATGATCCACAGACTGTC 660
QY 221 ThrAlaValAlaGlyValIleValSerTyrProPheAspThrValArgArgMetMet 240
Db 661 ACTGCTGTGGGGGCTGACTTCTTATCCATTTGACACCGTTCGCGCGCATGATGAGT 720
QY 241 GlnSerGlyArgGlyValAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260
Db 721 CAGTACGGGCGCAAGAGAACTGACATCATGTACAGAGGACGCTTACGTGCGGGAAG 780
QY 261 IlePheArgAspGluGlyGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuArg 280
Db 781 ATTCCTCTGATGAGAGAGGCAAAAGCTTTTTCAGAGGTGATGATGATGATGATGAT 840
QY 281 GlyMetGlyGlyAlaPheValIleuValIleuTyrAspGluLeuLysValIle 296
Db 841 GGCATGGGT 888

RESULT 4

US-08-961-871-9
; Sequence 9, Application US/08961871
; Patent No. 6013858
; GENERAL INFORMATION:
; APPLICANT: Wallace, Douglas C.
; APPLICANT: Graham, Brett H.
; APPLICANT: Macgregor, Grant R.
; TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine
; TITLE OF INVENTION: Nucleotide Translocator Protein and Methods
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/961.871
FILING DATE: 31-OCT-1997
CLASSIFICATION: 800
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/030,017
FILING DATE: 01-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 78-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8089
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1177 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: not relevant
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: 94..990
US-08-961-871-9

Alignment Scores:
Pred. No.: 1,566-163 Length: 1177
Score: 1412.00 Matches: 264
Percent Similarity: 94.97% Conservative: 19
Best Local Similarity: 88.59% Mismatches: 15
Query Match: 91.51% Indels: 0
DB: 3 Gaps: 0

US-09-811-094-33 (1-298) x US-08-961-871-9 (1-1177)

QY 1 MetThnGluglAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAlaAla 20
DB 94 ATGGGGATCAGCCTTGTAGCTTCTTAAGACTTCCTGCGAGGCGGCGCGCC 153

QY 21 IleSerIysThrAlaValAlaProIleGluArgValAlaLysLeuLeuGlnAlaGlnHis 40
DB 154 GTCTCCAGACCGCGCTGCGCCCGCATGAGAGGGTCAAACTGCTGCTCAGGTCACCAT 213

QY 41 AlaserIysGlnIleAlaAlaAspLysGlnIleValAlaValAlaValAlaValAla 60
DB 214 GCCAGCAACAGATCAGTCAAGACAGACAGTACAAAGCATCATGATTGTGCTGAGA 273

QY 61 IleProIysGlnIleAlaLysLeuSerPheThrArgGlyAlaValAlaValAlaValAla 80
DB 274 ATCCCAAGAGAGAGGCTTCTCTCTCTGAGAGGGTACCTGCGCAAGTATCGG 333

QY 81 TyrPheProThrAlaAlaLeuAsnPheAlaPheLysAspLysIleValAlaValAla 100
DB 334 TACTTCCCACTCAAGCCCTGAACTTCCTTCAAGACAGTACAGACATCTCTCG 393

QY 101 GlyIleValAlaAspLysIleThrGlnPheThrArgTyrPheAlaGlyAlaValAlaValAla 120
DB 394 GGAGGCGTATGACATAGCATGAGTTCGCGGCTGCTTCTCTGTAACCTGCGCTCTGCT 453

QY 121 GlyAlaAlaGlyAlaThrSerLeuLysPheValIleProLeuAspPheAlaValAlaValAla 140
DB 454 GGGGAGAGTGGGCGACCTCCCTGCTGCTGCTTCAAGCGTGAAGCTTCTGAGCAGC 513

QY 141 LeuAlaAlaAspValAlaGlyLysSerGlyThrGlnArgGlnPheArgGlyLeuGlyAlaValAla 160
DB 514 CTGGGTGGGAGCGTGGGCAAGGATCTCCACGAGAAATTCATGAGGCTGGGCGACATGT 573

QY 161 LeuValAlaValIleThrLysSerAspGlyIleAlaGlyLeuValArgGlnGlyPheSerValSer 180
DB 574 CTCACCAAGATCTTCAAGTCCGAGCGCTGAAGGGGTCTTACCGAGGTTTCAAGTGTCTCT 633

QY 181 ValGlnGlyIleIleIleIleTyrArgAlaAlaTyrPheGlyAlaTyrAspThrAlaLysGly 200
DB 634 GTCCAGGGCATCATCATCTACAGAGCTGCTTCCGAGTCTATGACCTGCAAGGG 693

QY 201 MetLeuProAspProLysAsnThrHisIleValSerTrpMetIleAlaGlnThrVal 220
DB 694 ATGCTCCAGACCCCAAGATGACATTCGACATTCGACCTGATGATGCCAGATGTG 753

QY 221 ThrAlaValAlaGlyAlaValSerTyrProPheAspThrValAlaGArgMetMet 240
DB 754 ACAGCGGTGGGCGGCTGCTCTTATCCGTTGACACTGTCCTGATAGAGATGATG 813

QY 241 GlnSerGlyAlaGlyAlaAspIleMetIleTyrThrGlyThrValAspCysTrpArgLys 260
DB 814 CAGTGTGGCCCAAGGGGCTGATATTATGATACCGGAGACATTCGCTGAGAGAG 873

QY 261 IlePheArgAspGluGlyAlaPhePheLysGlyAlaIleTyrPheAspValAlaValAla 280
DB 874 ATTGCAAAAGATGAAGAGCCACGCTTCTTCAAGGTCTGCTGCTCATGATGATG 933

QY 281 GlyMetGlyIleAlaPheValLeuValLeuTyrAspGluLeuLysValIle 298
DB 934 GCCATGGTGTGCTTTGTATGTGTATGATGATGATCAAAAATATGTG 987

RESULT 5
US-08-961-871-11
Sequence 11, Application US/08961871
Patent No. 6013858
GENERAL INFORMATION:
APPLICANT: Wallace, Douglas C.
APPLICANT: Graham, Brett H.
APPLICANT: MacGregor, Grant R.
TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine
TITLE OF INVENTION: Nucleotide Translocator Protein and Methods
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSER: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,871
FILING DATE: 31-OCT-1997
CLASSIFICATION: 800
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/030,017
FILING DATE: 01-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 78-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8089
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1259 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: not relevant
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 190..1086

Thu Aug 28 08:34:56 2003

us-09-811-094-33.p2n.inl

Page 6

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Db      538  GTCCAGGACATCATATCTATAGACTGCTACTTCGGAGCTATGATCTCCAGGCGG 597
OY      201  MetleuproaspProlysasnthrhslleValalserTrpmetlleaIacInthrVal 220
Db      598  ATGCGCTGACCCCAAGAACGTCACATTTTGTGAGCGATGATGCCAGGTGTG 657
OY      221  ThrIaValaIaagIyValserTyTrpPheaspThrValaIrgarIgmMetMet 240
Db      658  ACGGAGTCGCGAGGCGTGTCTACCCCTTTCACACTGTGCTGTGATGATGATG 717
OY      241  GlnSerGlyArgIySGlyAlaAspIleMetTyThrGlyThrValaSPcystTrpArg 260
Db      718  CAGTCCGCGCGAAGAGGCGCATATATGATACAGGGGACAGTGTGCTGGAGAG 777
OY      261  IlePheArgAspGluGlyGlyAlaPhePheIySGlyAlaTrpSerAsnValleuArg 280
Db      778  ATTGCAAAAGACGAGAGCCAGGCGCTTCGAAAGGTGCTGCTCCAAATGTCTGAGA 837
OY      281  GlyMetGlyGlyAlaPheValleuValleuTyraSPgluLeuIySGlyValIle 298
Db      838  GCGATGGCGGCTGCTTTGATTGTGCTGTATGATGATGATGATGATGATGCT 891

RESULT 7
US-09-996-243-288
: Sequence 288, Application US/09996243
: Patent No. 6478825
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: APPLICANT: Baker, Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferreira, Napoleone
: APPLICANT: Fong, Sherman
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gertlisen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Kijavlin, Ivar J.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tamas, Daniel
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2730P1C13
: CURRENT FILING DATE: 2001-11-13
: PRIOR APPLICATION NUMBER: US/09/996,243
: PRIOR FILING DATE: 1997-06-16
: PRIOR APPLICATION NUMBER: 60/062250
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/065186
: PRIOR FILING DATE: 1997-11-12
: PRIOR APPLICATION NUMBER: 60/065311
: PRIOR FILING DATE: 1997-11-13
: PRIOR APPLICATION NUMBER: 60/066770
: PRIOR FILING DATE: 1997-11-24
: PRIOR APPLICATION NUMBER: 60/075945
: PRIOR FILING DATE: 1998-02-25
: PRIOR APPLICATION NUMBER: 60/078910
: PRIOR FILING DATE: 1998-03-20
: PRIOR APPLICATION NUMBER: 60/083322
: PRIOR FILING DATE: 1998-04-28
: PRIOR APPLICATION NUMBER: 60/084600

: PRIOR FILING DATE: 1998-05-07
: PRIOR APPLICATION NUMBER: 60/087106
: PRIOR FILING DATE: 1998-05-28
: PRIOR APPLICATION NUMBER: 60/087607
: PRIOR FILING DATE: 1998-06-02
: PRIOR APPLICATION NUMBER: 60/087609
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: PRIOR APPLICATION NUMBER: 60/087759
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: PRIOR APPLICATION NUMBER: 60/088217
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: PRIOR APPLICATION NUMBER: 60/088655
: PRIOR FILING DATE: 1998-06-09
: PRIOR APPLICATION NUMBER: 60/088734
: PRIOR FILING DATE: 1998-06-10
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: PRIOR FILING DATE: 1998-06-10
: PRIOR APPLICATION NUMBER: 60/088824
: PRIOR FILING DATE: 1998-06-10
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: PRIOR FILING DATE: 1998-06-11
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: PRIOR APPLICATION NUMBER: 60/089105
: PRIOR FILING DATE: 1998-06-12
: PRIOR APPLICATION NUMBER: 60/089440
: PRIOR FILING DATE: 1998-06-16
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: PRIOR APPLICATION NUMBER: 60/089514
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: PRIOR APPLICATION NUMBER: 60/089598
: PRIOR FILING DATE: 1998-06-17
: PRIOR APPLICATION NUMBER: 60/089599
: PRIOR FILING DATE: 1998-06-17
: PRIOR APPLICATION NUMBER: 60/089600
: PRIOR FILING DATE: 1998-06-17
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PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-26
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PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978

PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Pred. No.:	2,98e-28	Length:	3334
Score:	314.00	Matches:	92
Percent Similarity:	50.68%	Conservative:	58
Best Local Similarity:	31.08%	Mismatches:	115
Query Match:	20.35%	Indels:	32
DB:	4	Gaps:	10

US-09-811-094-33 (1-298) x US-09-996-243-288 (1-3334)

QY 10 LysAspPheLeuAlaGlyIleAlaAlaIleSerIysThrAlaValaIleProIle 29
Db AGACACCTGGTGGCAGAGGTGGGGCGGCTATCCAGAACCTGCACAGGCCCTG 681

QY 30 GluArgValIysLeuLeuGlnValGlnHisAlaSerIysGlnIleAlaIleAspIys 49
Db GACAGGCTCAAGGTGCTCATGCAGTCC---CATGCTCCGC-----AGC 723

QY 50 GlnIysGlyIleValaIleAspCysIleValaIleProIysGlnIleValaIleSer 69
Db AACACATGGGCGATGCTGGTGGCTTCACTCATGATGTCGAGAGAGGGCCAGGTCA 783

QY 70 PheTyrArgIysLeuAlaAsnValIleArgTyrPheProThrGlnAlaLeuAspPhe 89
Db CTCTGGCGGGGCGATGCATCAACGTCCTCAAAATGCCCCCGAATCCAGCATCAATTC 843

QY 90 AlaPheIysAspIysTyrIysGlnIlePheLeuGlyIleValaIleAspIysHisThrGlnPhe 109
Db ATGGCCATAGCAGCATCAAGCC-----CTGTGTGGTGTGATCCAGAGACT----- 891

QY 110 TrpArgTyrPheAlaGlyAlaLeuAlaSerGlyIleAlaAlaIleAlaIleThrSerLeuCys 129
Db ---CTGAGATTCACGAGAGGCTTGGCGAGGCTTGGCAGAGGCCATCGCCAGAGC 948

QY 130 PheValTyrProIleAspPheAlaArgTyrArgLeuAlaAlaAspValGlyIysSerGly 149
Db AGCATCTACCCATGAGGAGTCTGAAAGCCGAGTGGCG-----CTGCGGAAGACAGGC 1002

QY 150 ThrGluArgIleuPheArgIysLeuGlyAspCysLeuValIysIleThrIysSerAspGly 169
Db 1003 -----CAGTACTCAGGAATGCTGATGCGCCAGAGGATCTCGCCAGAGAGGG 1053

QY 170 IleArgGlyLeuTyrGlnIysPheSerValSerValGlnIysIleIleIleTyrArgAla 189
Db 1054 GTGGCGCCTTCTACAAAGGCTATGTCCTCCACATGCTGGGATCATCCCTATGCCGGC 1113

QY 190 AlaTyrPheGlyValTyrAspThrAlaIysGlyMet----- 201
Db 1114 ATCGACCTTCACATTCAGAGAGCTTCACAAATGCCGCTGCAGACATATGACGTGAC 1173

QY 202 LeuProAspProIysAsnThrHisIleValVal-SerTrpMetIleGlnIleThrValTh 221
Db 1174 AGCGCGGAGCC-----GGCGTGTGTGCTCTGCGCTGTGACACATGTCAGT 1224

QY 221 AlaValAlaGlyValValSerTyrProPheAspThrValaIleArgIysMetMetGly 241
Db 1225 ACCTGTGGCCAG---CTGGCAGAGTACCCCGCGCCCTAGTCAGAGCCGAGTGCAGGGCA 1283

QY 241 nserGlyArgIysGlyAlaAspIleMetTyrThrGlyThValaIleAspCysTrpArgIysIle 261
Db 1284 AGCCTATATGAGGGCGCTCCGAGGAGCATATGAGCAGCCTC-----TTCAAAACATAT 1337

QY 261 ePheArgAspGlnIleGlyIysAlaPhePheIysGlyAlaIleTrpSerAsnValIleValGly 281
Db 1338 CTCTGGGACCGAGAGGGGCTTGGGCGCTGTACAGGGGCTGGCCCACTTCTATGAAGGT 1397

QY 281 yMetGlyIleAlaPheVal---LeuValIleuTyrAspGluLeuIys 295

[illegible]

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Db      1115 ATGCACCTAGCTGTCTATGACACATTTG-----ValValserTprmetilleagin 218
OY      210 Ile-----|||
Db      1154 CTCACGGCTACCGACTAAACAGTCAGACCCGGGTTGTCGTCCTCCGCGCTGTGT 1213
OY      219 ThrValThrAlaValAlaGly---ValValserTyrProPheAspThrValAlaArgAlaArg 237
Db      1214 ACTATCTCCAGTACTCTTGTCGGCAGCTGCGACCTGCACAGCTACCCACATAGCCCTGTCAGACCGG 1273
OY      238 MetMetMetInserylValArgGlyValAspIleMetTyrThrGlyThrValAlaPcys 257
Db      1274 ATGGAGGCACAAACCCCTCCATTGTAGGGGCGCACCTGAGATACCATGACGACGCTTC----- 1327
OY      258 TprArgIysIlePheArgAspGluGlyGlyValAlaPhePheIysGlyAlaIATPserAsn 277
Db      1328 TTCAAAACAGATTTCTGGCGACTGAGGGCGCCCTTTGGCTCTACCGGGGGCTGGCCCCAAC 1387
OY      278 ValIeuArgIyMetGlyValAlaPheVal---LeuValIleuTyrAspGluLeuIys 295
Db      1388 TTCATGAGAGTGATCCCGGCTGTGAGCATCAGCTACGTAGTGTCTACGAAACCTGGAAG 1444

RESULT 9
US-09-312-283C-262
Sequence 262, Application US/09312283C
Patent No 6573095
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishnamand D.
TITLE OF INVENTION: Compositions isolated from skin cells
FILE REFERENCE: 11000.1011c2
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 262
LENGTH: 1816
TYPE: DNA
ORGANISM: Mouse
US-09-312-283C-262

Alignment Scores:
Pred. No.: 2,82e-28 Length: 1816
Score: 311.00 Matches: 88
Percent Similarity: 50.17% Conservative: 62
Best Local Similarity: 29.43% Mismatches: 111
Query Match: 20.16% Indels: 38
Gaps: 11

US-09-811-094-33 (1-298) x US-09-312-283C-262 (1-1816)
OY      10 LysAspPheLeuAlaGlyIyIleAlaAlaAlaIleSerLysThrAlaValAlaProIle 29
Db      623 AGGCACCTGTGTGCGACGAGGTGGGCGAGGGCGAGTTTCCAGAACCTGCACCTGCCCCCTG 682
OY      30 GluArgValIysLeuLeuIeuGlnValGlnHisAlaSerLysGlnIleAlaAlaAspLys 49
Db      683 GACGAGCTAAGTGTCTATCAGAGTCT---CATGTGCTCCGCC-----AGC 724
OY      50 GluTyrIyGlyIleIleValAspCysIleValArgIleProLysGluGlnIyValIeuSer 69
Db      725 AACAAACATGTGCATGCTGTAGTGTGATTCACACAGATGATTCACAGAAAGGGGACCAAGTCA 784
OY      70 PheThrArgGlyAspLeuAlaAsnValIleAcGlyTyrPheProThrGlnAlaIeuAsnPhe 89
Db      785 CTCTGGGGGGGCAACGCGATCAATATCTCTCAAAATTTGGCCCTGTAGCTGGCGCATCAAAATTC 844

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QY 90 AlaphelysAspLysTrpLysGlnIlePheLeuGlyGlyValAspLysHisThrGlnPhe 109
 Db 845 AAGCATATAGCAGATGAAACGG-----CTTGTCCAGTACAGACAGAGC----- 892
 QY 110 TPrpArgTyPheAlaGlyAsnLeuAlaSerGlyGlyAlaAlaGlyAlaThrSerLeuGly 129
 Db 893 ---CTGAGATATCCAGAAAGGCTTGTGGAGGCTCTTGGCCGAGCAATTGCCAGAGT 949
 QY 130 PheValIleTyPProLeuAspPheAlaArgThrArgLeuAlaAlaAspValGlyLysSerGly 149
 Db 950 AGCATCTACCAATGAGAGTCTGAAAGACCCGAAATGCC-----CTGGGAAACAGGA 1003
 QY 150 ThrGlnArgGlnPheArgGlyLeuGlyAspCysLeuValLysIleThrLysSerAspGly 169
 Db 1004 -----CAGTACTCCGCGCATGTGAGTGTGCGCAGAGATCTTGGCTAAAGAGGT 1054
 QY 170 IleArgGlyLeuTyGlnGlyPheSerValSerValGlnGlyIleIleIleTyArgAla 189
 Db 1055 GTAGCTGCTTCTACAAAGGCTACATCCCAACATGCTGGGATCATCCCTTATGCTGGC 1114
 QY 190 AlaTyPheGlyValIleTyAspThrAlaLysGlyMetLeuProAspProLysAsnThrHis 209
 Db 1115 ATCGACCTAGCTGTATGACATATG-----AAATATACCTGG 1153
 QY 210 Ile-----ValIleSerTrpMetIleAlaGln 218
 Db 1154 CTCACAGCGCTACGAGTAACAGTCAGACAGCCCGGTGTGTGCTGCTGCGCTGTGGT 1213
 QY 219 ThrValThrAlaValAlaGly---ValValSerTyProPheAspThrValArgArg 237
 Db 1214 ACTATCTCCAGTACTTGTGGCCAGCTGCGCAGCTACCCAGCTGCTGTGCTGAGACCGG 1273
 QY 238 MetMetMetGlnSerIleArgLysGlyAlaAspIleMetTyThrGlyThrValAspCys 257
 Db 1274 ATCGAGGCGACAAAGCCTCCATGAGGCGCAGCCTGAGTAACCATGACGAGCCTC----- 1327
 QY 258 TrpArgLysIlePheArgAspGlnGlyGlyLysAlaPhePheLysGlyAlaTrpSerAsn 277
 Db 1328 TTCAAACACATCTCTGAGGAGCTGAGGCGGCTTGGGCTTACCGGGGGGCGCCCAAC 1387
 QY 278 ValLeuArgGlyMetGlyGlyAlaPheVal---LeuValLeuTyAspGlnLeuLys 295
 Db 1388 TTCATATAGGTATTCGCCGCTGTGAGCATACGCTACGTGTGTACGAAACCTGGAAG 1444
 RESULT 10
 US-09-620-312D-283
 : Sequence 283, Application US/09620312D
 : Patent No. 6569662
 : GENERAL INFORMATION:
 : APPLICANT: Tang, Y. Tom
 : APPLICANT: Liu, Chenghua
 : APPLICANT: Asundi, Vinod
 : APPLICANT: Zhang, Jie
 : APPLICANT: Ren, Feiyang
 : APPLICANT: Chen, Rui-hong
 : APPLICANT: Zhao, Qing A.
 : APPLICANT: Wehrman, Tom
 : APPLICANT: Xue, Aifong J.
 : APPLICANT: Yang, Yonghong
 : APPLICANT: Wang, Jian-Rui
 : APPLICANT: Zhou, Ping
 : APPLICANT: Ma, Yundong
 : APPLICANT: Wang, Dunrui
 : APPLICANT: Wang, Zhilwei
 : APPLICANT: John Tillinohast
 : APPLICANT: Drmanac, Radoje T.
 : TITLE OF INVENTION: No. 6569662el Nucleic Acids and
 : FILE REFERENCE: Polypeptides
 : CURRENT APPLICATION NUMBER: US/09/620,312D
 : PRIOR FILING DATE: 2000-07-19
 : PRIOR APPLICATION NUMBER: 09/552,317
 : PRIOR FILING DATE: 2000-04-25

: PRIOR APPLICATION NUMBER: 09/488,725
 : PRIOR FILING DATE: 2000-01-21
 : NUMBER OF SEQ ID NOS: 1105
 : SOFTWARE: PL_FL_genes Version 1.0
 : SEQ ID NO 283
 : LENGTH: 2663
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: (115)..(2157)
 US-09-620-312D-283
 Alignment Scores:
 Pred. No.: 1,28e-26 Length: 2663
 Score: 299.50 Matches: 88
 Percent Similarity: 44.85% Conservative: 47
 Best Local Similarity: 29.24% Mismatches: 139
 Query Match: 19,41% Indels: 27
 Gaps: 9
 US-09-811-094-33 (1-298) x US-09-620-312D-283 (1-2663)
 QY 4 GlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAlaIleSerLys 23
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 QY 24 ThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHisAlaSerLys 43
 Db 1144 ACTGACGTGATCTATAGTCTGTGTGAAGACCCGAAATGCAACACAGCTGCTGTGGC 1203
 QY 44 GlnIleAlaAlaAspLysGlnTyLysGlyIleValAspCysIleValArgIleProLys 63
 Db 1204 TCGTGTGTGGGAGCTAATGTACAAACAGCTTGTGACTTTTAAAGAAAGCTTGCT 1263
 QY 64 GluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArgTyPhePro 83
 Db 1264 TATGAGGCGCTCTTGTGACTCTACAGGGGTCTATACACACTTATAGGGGTGCTCCA 1323
 QY 84 ThrGlnAlaLeuAsnPheAlaPheLysAspLysTyLysGlnIlePheLeu 100
 Db 1324 GAAAGCCATTAATACTGACTGTAAATGATTTGTTGGGCAAAATTTACCAAGAGAT 1383
 QY 101 GlyGlyValAspLysHisThrGlnPheTrpArgTyPheAlaGlyAsnLeuAlaSerGly 120
 Db 1384 GGCTGCTGTCCA-----CTTCACACAGAGTCTTGCTGGA 1419
 QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyPProLeuAspPheAlaArgThrArg 140
 Db 1420 GGCTGTGCTGAGGCTCTCAGTCATTTTCCACCAACCATTTGAGATAGTGAAGATTCGT 1479
 QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGlnArgGlnPheArgGlyAspCys 160
 Db 1480 CTCGAAAGTA---GCTGAGAGATCACCCGAGCCAGAGCTACGCGCTG----- 1527
 QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyGlnGlyPheSerValSer 180
 Db 1528 -----AAGTGTGCTCGGAGCTTGGGAATTTTGTCTGTATAGAGGTGCCAAGCTGT 1581
 QY 181 ValGlnGlyIleIleIleTyArgAlaAlaTyPheGlyValTyAspThrAlaLysGly 200
 Db 1582 TTCCTCCGAGACATTCCTCTGCAATATTTCTCTTATGTCATTCCAAACTA 1641
 QY 201 MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220
 Db 1642 CTTCGTGCTGAT---GAAATGACACAGCGGAGTTTAAATCTTCTGCA-----GCT 1692
 QY 221 ThrAlaValAlaGlyVal-----ValSerTyPProPheAspThrValArgArg 236
 Db 1693 GAGCGCATGCGAGGTGCCAGCTGCATCTGTGTGACCCCTGTATGTATCATCAAGACA 1752
 QY 237 ArgMetMetMetIleSerGlyArgGlyAlaAspIleMetTyThrGlyThrValAsp 256
 Db 1752

Thu Aug 28 08:34:56 2003

us-09-811-094-33.p2n.rn1

Page 10

DB 1753 AGA-----CTGCAGTGTGCTGCCCGCTGCGCAGACATACAGTGTGTCATCGAC 1806
QY 257 CysrtparqlysllepharqaspgluqlysllysaAlaphepelysglyAlatrpser 276
DB 1807 TGTTCAGAGAAATTCCTCGGAGAAAGGCCCTCAGCATTTGGAAAGGAGCTCGAGCT 1866
QY 277 AsnValleuAarglyMetgylgyl--AlapheValleuValleuYraspgluLeuY 295
DB 1867 CGAGGTTCATGCTCTCTCCCGAGTTGTGTGTACCTTGCTACTATGAAAGTTCGAG 1926
QY 296 Lys 296
DB 1927 CGG 1929
RESULT 11
US-09-016-434-622
; Sequence 622, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; FILING DATE: HEREMITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 622:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 289 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LIVERU04
; CLONE: 2517151
US-09-016-434-622
Alignment Scores:
Pred. No.: 2,239-27 Length: 289
Score: 294.00 Matches: 65
Percent Similarity: 98.488 Conservative: 0
Best Local Similarity: 98.488 Mismatches: 1
Query Match: 19,058 Indels: 1
DB: 4 Gaps: 0
US-09-811-094-33 (1-298) x US-09-016-434-622 (1-289)
QY 1 MetHrGlucInAlaIleSerPheAlaLysAspPheLeuAlaGlyIleAlaIala 20

DB 93 ATGACGAGACAGCCATCTCTCTCCGCAAGACTTCTTGCGGAGGATCGCGCGCC 152
QY 21 lleserlystrAlaValAlaProIleGluAargValyleuLeuLeuGlnValGlnHis 40
DB 153 ATCTCCAGAGAGCGCGCTGCTCAGTCAGCGGCTCAGCTCTCTCTCAGAGTCAGAC 212
QY 41 AlaserlyslInleAlaAlaAspLysGlnTylyGlyIleValAlaPcyAlleValArg 60
DB 213 GCCAGCAAGCAGATCGCGCGCAGCAAGCAGATGAGGAGATGCTGATGAT -GTCCGC 271
QY 61 lleProLysGluIngly 66
DB 272 ATCCCAAGAGCAGCGCGC 289
RESULT 12
US-09-482-273-26
; Sequence 26, Application US/09482273
; Patent No. 6534631
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 71 Human secreted Proteins
; FILE REFERENCE: P2030P1
; CURRENT FILING DATE: 2000-01-13
; EARLIER FILING DATE: 1999-07-14
; EARLIER APPLICATION NUMBER: PCT/US99/15849
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,922
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,956
; NUMBER OF SEQ ID NOS: 267
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 1674
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1663)
; OTHER INFORMATION: n equals a,t,c,g, or c
US-09-482-273-26
Alignment Scores:
Pred. No.: 2,99-25 Length: 1674
Score: 286.00 Matches: 87
Percent Similarity: 45.678 Conservative: 50
Best Local Similarity: 29.008 Mismatches: 133
Query Match: 18,548 Indels: 30
DB: 4 Gaps: 8
US-09-811-094-33 (1-298) x US-09-482-273-26 (1-1674)
QY 10 LysAspPheLeuAlaGlyIleAlaAlaIleSerlystrAlaValAlaProIle 29
DB 332 AAACCTTGTGTATGATGGGCGCTCTCTATCGTGGCTTTGGAGACTTCCCTGTG 391
QY 30 GluArgValLysLeuLeuGlnValGlnHisAlaser-----LysGln 44
DB 392 GACCTTACCAAAACACGACTTCAGTTCAGGCCCAAGCATTTGATGCCCTTCCAAAGAG 451
QY 45 lIleAlaAlaAspLysGlnTylyGlyIleValAlaPcyAlleValArgIleProLysGlu 64
DB 452 ATA-----AAATATAGAGGATGTCATGCGCTTTTCGCATCTGTAAAGAG 499
QY 65 GlnGlyValleuSerPheTrpArgGlyAsnLeuAlaAsnValIleArgTyPheProThr 84
DB 500 GAAGGTGTATGCTCTCTATTCAGGATTCCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 559
QY 85 GluAlaLeuAsnPheAlaPheLysAspLysGlnIlePheLeuGlyIleValAlaP 104


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Db      560 GGCACCATTAATAATGGGATTTACCAAGCTTGACCCCTTATTCGTACAGCTTTAGAA 619
QY      105 LysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGlyGlyAlaAlaGly 124
Db      620 GATGAACACT-----CTTTAATTAATATGATCTGTGGGGTAGTGCAGGA 664
QY      125 AlaThrSerLeuGlyCysPheValTyrProLeuAspPheAlaArgThrArgLeuAlaAlaAsp 144
Db      665 GTGATTCCTTCACACTATACCAATCCACCGATGTTCTAAGATTCGAATGCAGGCT--- 721
QY      145 ValGlyLysSerGlyThrGlnArgGlnPheArgGlyLeuGlyAspGlyAspGlyLeuValLysIle 164
Db      722 -----CAAGGAAGCTTTGTTCCAAAGGACATGATGGAAAGC---TTTATCGATATA 769
QY      165 ThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSerValGlnGlyIle 184
Db      770 TACCAACAGAAAGGACCAAGGCGGTCTGTGGAGGGGTGTGGTTCACACTGCTCAGCGCT 829
QY      185 IleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLys----- 199
Db      830 GCCATGCTGTAGAGCTAGACGTACCAAGCTATGATATTAATAAGCAAGCATTTAATATTG 889
QY      200 ---GlyMetLeuProAspProLysAsnThrHisIleValSerThrMetIleAlaGln 218
Db      890 TCGAATATGATGGCGCATACATTTTAACCTACTGCTGTCCAGCTT----- 937
QY      219 ThrValThrAlaValAlaGlyValSerTyrProPheAspThrValArgArgMet 238
Db      938 ACATGTGGTTGGCTGGGCGCTCGCCCTCAACCCGGTGTGATGGTGCAGACTCGCATG 997
QY      239 MetMetGlnSerGlyArgGlyGlyAlaAspIleMetTyrThrGlyThrValAspCysTrp 258
Db      998 ATGAACCAAGAGGCAATCGTGGGACATGTGATCTGTATTAAGGCACTGTGTGATGTATT 1057
QY      259 ArgLysIlePheArgAspGlnGlyGlyLysAlaPhePheLeuValLeuTyrAspAsnVal 278
Db      1058 TTTAAATATGTGAAACATGAGGCTTTTTCACCTCATTAAGCAATTTTGGCCAAACTGG 1117
QY      279 LeuArg---GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGlnLeuLysVal 297
Db      1118 CTTCGGCTTGACCCCTGGAACATCATTTTATTATATACAGACAGCATTAAGAGGCTT 1177

RESULT 13
US-09-501-558-1
; Sequence 1, Application US/09501558
; Patent No. 6403784
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6403784e1 Human Uncoupling Proteins and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0012-USA
; CURRENT APPLICATION NUMBER: US/09/501,558
; CURRENT FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 876
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-501-558-1

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Alignment Scores:

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Pred. No.:      2 24e-25      Length:      876
Score:          283.50      Matches:      87
Percent Similarity: 46.84%      Conservative: 54
Best Local Similarity: 28.90%      Mismatches: 129
Query Match:    18.37%      Indels:      31
DB:            4          Gaps:      9

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US-09-811-094-33 (1-298) x US-09-501-558-1 (1-876)

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QY      10 LysAspPheLeuAlaGlyIleAlaAlaAlaIleSerLysThrAlaValAlaProIle 29
Db      19 AAGCCGTTGTGTACGGGGGCGTGGCTTCATACAGCTAGGCGGTACATTCCAAATT 78
QY      30 GlnArgValLysLeuLeuGlnValGlnHisAlaSer-----LysGln 44
Db      79 GATTTAACCAAGACAGCGGCTCCAGATTTCAGAGCCAGACGATGATGCAAAATTTAAGGA 138
QY      45 IleAlaAlaAspLysGlnTyrLysGlyIleValAlaAspCysIleValArgIleProLysGlu 64
Db      139 ATT-----AGATACGAGGAATGTTCACCGCATTTAGTGAGGATAGGACAGAA 186
QY      65 GlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArgTyrPheProThr 84
Db      187 GAAGGGCTGAAGACACTACTACGCGGGATTGCCCGCGCATGTATAGCCAGCATCTAT 246
QY      85 GlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeuGlyIleValAsp 104
Db      247 GGCACCATCAAGATAGGCACTTACCAAGCTTACAGGCACTATTCATTTGAACGCCAGAA 306
QY      105 LysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGlyGlyAlaAlaGly 124
Db      307 GATGAACACT-----CTACCATTAATGTGATATGTGGAATTCGTCTGGA 351
QY      125 AlaThrSerLeuGlyCysPheValTyrProLeuAspPheAlaArgThrArgLeuAlaAlaAsp 144
Db      352 GTCATATCTTCACACCATGCTATACCAACGATGTTTGAATAATTCGATGCAAGCG--- 408
QY      145 ValGlyLysSerGlyThrGlnArgGlnPheArgGlyLeuGlyAspCysLeuValLysIle 164
Db      409 -----CAAGCAACACCATTTCAA-----GGAGGAATGTATAGCAACTTCATGAACATT 456
QY      165 ThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSerValGlnGlyIle 184
Db      457 TACCAAGACAGAGGAGACAGACAGCTGTGAAGGCTGTCCCTTACTCGCCAGAGGCT 516
QY      185 IleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLys----- 199
Db      517 GCTATTGTTGTGGTGTGAGAGCTGCCGCTATAGACATCAACAAAGACATCTATTCTC 576
QY      200 ---GlyMetLeuProAspProLysAsnThrHisIleValSerThrMetIleAlaGln 218
Db      577 TCAAGCCTGATGGAGACACTGTGTATATCCACTCTCTCAAGCTTC----- 624
QY      219 ThrValThrAlaValAlaGlyValSerTyrProPheAspThrValArgArgMet 238
Db      625 ACCGTGGTGTGGCAGGCGCCCTGGCTCAAAACCTGTGATGTGTGAGACACGTAAG 684
QY      239 MetMetGlnSerGly---ArgLysGlyAlaAlaAspIleMetTyrThrGlyThrValAspCys 257
Db      685 ATGATATCAGAGAGTGTGAGATGAGCATGTTCGTGCATACAGCAAGCAACCTCGAGATTGC 744
QY      258 TrpArgLysIlePheArgAspGlnGlyGlyLysAlaPhePheLysGlyAlaTrpSerAsn 277
Db      745 TTGTTCACAGACATGAAGATGAAGGCTTTTTCCTCTCTATTAAGGCTTTTGCCAAAT 804
QY      278 ValLeuArg---GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGlnLeuLysVal 296
Db      805 TGTGTGAGACTTGCTCTTGGAATATCATTTCTTTGTGCATATACGACGACTTGAAGAAA 864
QY      297 Val 297
Db      865 TTG 867

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RESULT 14

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US-09-160-119-3
; Sequence 3, Application US/09160119A
; Patent No. 6316219
; GENERAL INFORMATION:
; APPLICANT: SOUCHET, STEPHANE
; APPLICANT: SOUCHET, MICHEL
; APPLICANT: BRILL, ANTOINE

```

```

TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30985
CURRENT APPLICATION NUMBER: US/09/160,119A
CURRENT FILING DATE: 1998-09-24 97402511.6
EARLIER APPLICATION NUMBER: EP 98401655.0
EARLIER FILING DATE: 1997-10-23 98401655.0
EARLIER APPLICATION NUMBER: EP 98401655.0
EARLIER FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 1443
TYPE: DNA
ORGANISM: HOMO SAPIENS
US-09-160-119-3

Alignment Scores:
Pred. No.: 1,276-24 Length: 1443
Score: 280.00 Matches: 80
Percent Similarity: 43.05% Conservative: 47
Best Local Similarity: 27.12% Mismatches: 148
Query Match: 18.15% Indels: 20
Gaps: 6
DB: 4

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US-09-811-094-33 (1-298) x US-09-160-119-3 (1-1443)
OY 4 GlnAlaIleSerPheAlaLysAspPheLeuAlaGlyIleAlaAlaIleSerLys 23
DB 385 CAAGTTGCAGAGTGGCTACAGGTTGGTGGTCTGCTGAGAGCTGTGGAGCC 444
OY 24 ThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHisAlaSerLys 43
DB 445 ACTGCTGTATCTCTATGATGATCTGTGTAACACCAATCCAGAACCAACATCACTGCGC 504
OY 44 GlnIleAlaAlaAspLysGlnIleLysGlyIleAlaAspCysIleValAlaGlyLeuProLys 63
DB 505 TCTTTTGTGGAGACCTATGATATTAACACCTTGTGATCTGTTTAAGAAAGTCTACGC 564
OY 64 GluGlnGlyValLeuSerPheTrpArgLysAsnLeuAlaAsnValIleArgLysPhePro 83
DB 565 TATGAAGGCTTCTTGGACCTGATAGAGCTCTTCCACATTTATGGAGTGGCCCA 624
OY 84 ThrGlnAlaLeuAspPheAlaPheLysAspLysGlyIleAlaPheLeu----- 100
DB 625 GAGAGAGCCATTAACCTTACAGTACGATTTGTGAGGATTAATTTATGACAAAGAT 684
OY 101 GlyIleValAlaAspLysHisThrGlnPheTrpArgLysPheAlaGlyAsnLeuAlaSerGly 120
DB 685 GGTTCGGTCCCA-----CTTGCAGCAGAAATCTTGGCTGGA 720
OY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValLysProLeuAspPheAlaArgTrpArg 140
DB 721 GGGCTGCTGAGGCTCCAGGCTGATTTTCAAAATCTTTAGAAATGTCAGATCGCT 780
OY 141 LeuAlaAlaAspValGlyLysSerGlyThrGlnArgGlnPheArgGlyLeuGlyAspCys 160
DB 781 TTGGAGAGT---GCAAGGAAATTCACACCTGCTCCGAGTCAAGTCTCTG----- 828
OY 161 LeuValLysIleThrLysSerAspLysIleArgGlyLeuGlyGlnGlyPheSerValSer 180
DB 829 -----TCTCTGCTGGGACCTGGGGTTTTTGGGATCTACAAAGGTCACCAAGATCG 882
OY 181 ValGlnGlyIleIleIleTrpArgAlaAlaLysPheGlyValLysAspPheAlaIleGly 200
DB 883 TTTCTGGGAGCATTTCTTCTGCGCATCTACTTCTCCGCTGCTGCTGCTGCTGCTGCT 942
OY 201 MetLeuProAspProLysAsnThrHisIleValAlaSerTrpMetIleAlaGlnThrVal 220
DB 943 TCCCTTTCAGAAATAGATGCGAGGTAGCCAGAGAGCTGCTCTTACCTGCTGCTCA 1002
OY 221 ThrAlaVal---AlaGlyValAlaSerTrpPheAspPheValArgArgTrpMet 239
DB 1003 GCTGCTATGCTGCTGACATCTTATGAGACCTCTGCTGATCTTATTCAGACGAGA----- 1056

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OY 240 MetGlnSerGlyArgLysGlyAlaAspIleMetLysThrGlyThrValAspCysTrpArg 259
DB 1057 TTACAGGTGGCTGCGCGGCTGGCCAAACCACTTACAGCGGAGTATGACTGCTTAGA 1116
OY 260 LysIlePheArgAspGlnGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeu 279
DB 1117 AAGATACCTGCTGAGAGAGAGCAAAACCTCTGTGAGAGGAGCTGGCTGCTGATTT 1176
OY 280 ArgGlyMetGlyAlaPheValLeuValLeuTrpAspIleLeu 294
DB 1177 CGATCTACCCAGCTTGTGTTGCTTACTTGTCTGACTTACGAAATG 1221

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RESULT 15
US-09-160-119-1
; Sequence 1, Application US/09160119A
; Patent No. 6316219
; GENERAL INFORMATION:
; APPLICANT: KRIEF, STEPHANE
; APPLICANT: SOUCHET, MICHEL
; APPLICANT: BRIL, ANTOINE
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30985
; CURRENT APPLICATION NUMBER: US/09/160,119A
; EARLIER FILING DATE: 1998-09-24
; EARLIER APPLICATION NUMBER: EP 97402511.6
; EARLIER FILING DATE: 1997-10-23
; EARLIER APPLICATION NUMBER: EP 98401655.0
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2095
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-160-119-1

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Alignment Scores:
Pred. No.: 2,26-24 Length: 2095
Score: 280.00 Matches: 80
Percent Similarity: 43.05% Conservative: 47
Best Local Similarity: 27.12% Mismatches: 148
Query Match: 18.15% Indels: 20
Gaps: 6
DB: 4

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US-09-811-094-33 (1-298) x US-09-160-119-1 (1-2095)
OY 4 GlnAlaIleSerPheAlaLysAspPheLeuAlaGlyIleAlaAlaIleSerLys 23
DB 1037 CAAGTTGCAGAGTGGCTACAGGTTGGTGGTCTGCTGAGAGCTGTGGAGCC 1096
OY 24 ThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHisAlaSerLys 43
DB 1097 ACTGCTGTATCTCTATGATGATCTGTGTAACACCAATCCAGAACCAACATCACTGCGC 1156
OY 44 GlnIleAlaAlaAspLysGlnIleLysGlyIleAlaAspCysIleValAlaGlyLeuProLys 63
DB 1157 TCTTTTGTGGAGACCTATGATATTAACACCTTGTGATCTTTTAAGAAAGTCTACGC 1216
OY 64 GluGlnGlyValLeuSerPheTrpArgLysAsnLeuAlaAsnValIleArgLysPhePro 83
DB 1217 TATGAAGGCTTCTTGGACCTGATAGAGCTCTGTTGCCACAGTATTTAGGAGTGGCCCA 1276
OY 84 ThrGlnAlaLeuAspPheAlaPheLysAspLysGlyIleAlaPheLeu----- 100
DB 1277 GAGAGAGCCATTAACCTTACAGTACGATTTGTGAGGATTAATTTAGCAAAAGAT 1336
OY 101 GlyIleValAlaAspLysHisThrGlnPheTrpArgLysPheAlaGlyAsnLeuAlaSerGly 120
DB 1337 GGTTCGGTCCCA-----CTTGCAGCAGAAATCTTGGCTGGA 1372
OY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValLysProLeuAspPheAlaArgTrpArg 140

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: August. 27, 2003, 13:44:11 ; Search time 330 Seconds

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Title: US-09-811-094-33

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1533700 seqs, 1147125425 residues

Total number of hits satisfying chosen parameters: 3067400

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database : Published Applications.NA.*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1543	100.0	897 9	US-09-811-094-33 Sequence 3, Appl1

2	1543	100.0	897 9	US-09-810-644-3	Sequence 3, Appl1
3	1543	100.0	897 10	US-09-185-904A-3	Sequence 3, Appl1
4	1543	100.0	1212 14	US-10-037-270-687	Sequence 687, Appl
5	1510	97.9	2592 13	US-10-044-090-152	Sequence 152, App
6	1454	94.2	897 9	US-09-811-094-2	Sequence 2, Appl1
7	1454	94.2	897 9	US-09-810-644-2	Sequence 2, Appl1
8	1454	94.2	897 10	US-09-185-904A-2	Sequence 2, Appl1
9	1424	92.3	1196 10	US-09-917-800A-1327	Sequence 1327, Ap
10	1409	91.3	1711 14	US-10-198-846-13437	Sequence 13437, A
11	1385.5	89.8	894 9	US-09-811-094-1	Sequence 1, Appl1
12	1385.5	89.8	894 10	US-09-810-644-1	Sequence 1, Appl1
13	1385.5	89.8	894 10	US-09-185-904A-1	Sequence 1, Appl1
14	1356.5	87.9	1116 10	US-09-966-708-213	Sequence 213, App
15	1356.5	87.9	1116 10	US-09-880-107-2096	Sequence 2096, Ap
16	1356.5	87.9	1116 14	US-10-171-581-48	Sequence 48, Appl
17	1193	77.3 <td>2706 14</td> <td>US-10-103-313-611</td> <td>Sequence 611, App</td>	2706 14	US-10-103-313-611	Sequence 611, App
18	936	60.7	720 9	US-09-910-943-105	Sequence 105, App
19	760.5	49.3	957 10	US-09-801-368-251	Sequence 251, App
20	750.5	48.6	1158 10	US-09-938-842A-608	Sequence 608, App
21	750	48.6	468 11	US-09-918-995-26014	Sequence 26014, A
22	749.5	48.6	1536 9	US-09-734-569-169	Sequence 169, Appl
23	742.5	48.1	1493 9	US-09-770-445-7	Sequence 7, Appl1
24	737	47.8 <td>927 14</td> <td>US-10-128-714-2338</td> <td>Sequence 2338, Ap</td>	927 14	US-10-128-714-2338	Sequence 2338, Ap
25	737	47.8 <td>927 14</td> <td>US-10-128-714-7338</td> <td>Sequence 7338, Ap</td>	927 14	US-10-128-714-7338	Sequence 7338, Ap
26	734.5	47.6	1458 12	US-10-141-478A-1	Sequence 1, Appl1
27	708	45.9	501 9	US-09-833-790-161	Sequence 161, App
28	700	45.4	493 11	US-09-918-995-9153	Sequence 9153, Ap
29	698.5	45.3	2037 12	US-10-259-165-191	Sequence 191, App
30	683	44.3	858 14	US-10-198-846-9464	Sequence 9464, App
31	679	44.0	1186 14	US-10-128-714-1338	Sequence 1338, Ap
32	679	44.0	1186 14	US-10-128-714-5338	Sequence 5338, App
33	679	44.0	3185 14	US-10-128-714-5338	Sequence 6338, App
34	679	44.0	3186 14	US-10-128-714-5338	Sequence 5338, App
35	670	43.4	410 11	US-09-918-995-16539	Sequence 16539, A
36	658	42.6	417 11	US-09-918-995-1864	Sequence 1864, Ap
37	656	42.5	483 11	US-09-918-995-1495	Sequence 1495, Ap
38	649.5	42.1	464 9	US-09-864-761-1408	Sequence 1408, Ap
39	646	41.9	513 11	US-09-918-995-97948	Sequence 97948, A
40	640	41.5	485 11	US-09-918-995-8792	Sequence 8792, Ap
41	607	39.3	474 11	US-09-918-995-6148	Sequence 6148, Ap
42	607	39.3	484 11	US-09-918-995-6070	Sequence 6070, Ap
43	606	39.3	460 11	US-09-918-995-4700	Sequence 4700, Ap
44	594	38.5	434 10	US-09-960-352-12424	Sequence 12424, A
45	568	36.8	420 11	US-09-918-995-5524	Sequence 5524, Ap

ALIGNMENTS

RESULT 1
US-09-811-094-33
Sequence 3, Application US/09811094
Patent No. US20010044144A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Miller, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Pel, Yashong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088.420D4
CURRENT APPLICATION NUMBER: US/09/811, 094
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 897
TYPE: DNA
ORGANISM: Homo sapien

US-09-811-094-3

Alignment Scores:

Pred. No.:	2,32e-200	Length:	897
Score:	1543.00	Matches:	298
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-811-094-33 (1-298) x US-09-811-094-3 (1-897)

```
QY 1 MethrGlunGlnAlaIleSerPheAlaIysAspPheLeuAlaGlyIleAlaAla 20
  |||||||
DB 1 ATGACGGACAGCCATCTCTTCCGCAAGACTTCTGGCCGAGGACATCGCCGCC 60
QY 21 IleserIyThrAlaValAlaProIleGluArgValIysLeuLeuGlnValGlnHis 40
  |||||||
DB 61 ATCTCCAGAGCGCGCTGCTCCGATCCAGCGGCTCAAGCTGCTGCTGCGAGGTC 120
QY 41 AlaserIyGlnIleAlaAlaAspIyGlnIyIleValAspCyIleValArg 60
  |||||||
DB 121 GCCACAGAGATCGCGCCGACAGACGATACAGGCGCATCTGCACTGCTGCGC 180
QY 61 IleProIyGlnIyValIleuSerPheTrpArgIyAsnLeuAlaAsnValIleArg 80
  |||||||
DB 181 ATCCCAAGAGAGCGGCGCTGCTCTTCTGAGGGGCAACCTTGCCACGATTCGC 240
QY 81 TyrPheProTrhGlnAlaLeuAsnPheAlaPheIyAspIyTyIyGlnIlePheLeu 100
  |||||||
DB 241 TACTTCCCACTCAAGCCCTCAACTTCGCTCAAGGATTAAGTACAGAGATCTCTG 300
QY 101 GlyIyValAlaPlyShIerhGlnPheTrpArgIyPheAlaGlyAsnLeuAlaSerGly 120
  |||||||
DB 301 GGGGGCGGGGAGAGCGACGAGATCTGAGGATCTTGGGGCAACCTGCGCTCGGC 360
QY 121 GlyAlaIleAlaGlyAlaTrhSerLeuCySpheValTyIProLeuAspPheAlaTrhArg 140
  |||||||
DB 361 GGTGGGGCGGGGAGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 141 LeuAlaIleAspValIyIySerGlyTrhGluArgIyPheArgIyLeuGlyAspCyS 160
  |||||||
DB 421 CTGGCAGCGGAGCGTGGGAAAGTCAGGACAGAGCGGATTCGAGGCTCGAGACTGC 480
QY 161 LeuValIyIleIleTrhIySerAspGlyIleArgGlyLeuTyIyGlnIyPheSerValSer 180
  |||||||
DB 481 CTGGTGAAGATCAACCAAGTCGAGGCGATCCGGGGCTGTACAGGGCTTCAGTCTCC 540
QY 181 ValGlnGlyIleIleIleTyIArgAlaAlaTyIyPheGlyValIyAspTrhAlaIySgIy 200
  |||||||
DB 541 GTCCAGGCGATCATCTACCGGCGGCTTACTTGGCGTACGATACGCGCAAGGGC 600
QY 201 MetLeuProAspProIyAsnTrhHisIleValIySerTrpMetIleAlaGlnTrhVal 220
  |||||||
DB 601 ATCTCTCCCGACCCCAAGACACGACATCGTGGTGAAGTATGATCGCGAGACCGTG 660
QY 221 ThrAlaValAlaGlyValIyValSerTyIProPheAspTrhValArgArgMetMetMet 240
  |||||||
DB 661 ACGGCGGTGGCGGTGGTGTCTTCTTACCTTCTGACACGCTGGCGGCGATATATG 720
QY 241 GlnSerGlyArgIyGlyAlaAspIleMetTyITrhGlyTrhValAspCySerTrpArgIyS 260
  |||||||
DB 721 CAGTCCGGCGGCAAGAGAGCTGATCATGTACACGCGGACCGTGAATGTTGAGAGAG 780
QY 261 IlePheArgAspGlyGlyIyValAlaPhePheGlyGlyAlaTrpSerAsnValIleArg 280
  |||||||
DB 781 ATCTTCAAGATGAGAGGGGCGAGGCGCTTCTTCAAGGATGCTGATCAAGTCTCTCGG 840
QY 281 GlyMetGlyGlyAlaPheValIleuValIleuTyIAspGlyLeuIyValIle 298
  |||||||
DB 841 GGGTGGGGGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 894
```

RESULT 2

US-09-810-644-3

Sequence 3, Application US/09810644

Patent No. US20020012992A1

GENERAL INFORMATION:

```
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Wiley, Scott W.
APPLICANT: Szabo, Thomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
FILE REFERENCE: 660088.420D3
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 897
TYPE: DNA
ORGANISM: Homo sapien
```

US-09-810-644-3

Alignment Scores:

Pred. No.:	2,32e-200	Length:	897
Score:	1543.00	Matches:	298
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-811-094-33 (1-298) x US-09-810-644-3 (1-897)

```
QY 1 MethrGlunGlnAlaIleSerPheAlaIysAspPheLeuAlaGlyIleAlaAla 20
  |||||||
DB 1 ATGACGGACAGCCATCTCTTCCGCAAGACTTCTGGCCGAGGACATCGCCGCC 60
QY 21 IleserIyThrAlaValAlaProIleGluArgValIysLeuLeuGlnValGlnHis 40
  |||||||
DB 61 ATCTCCAGAGCGCGCTGCTCCGATCCAGCGGCTCAAGCTGCTGCTGCGAGGTC 120
QY 41 AlaserIyGlnIleAlaAlaAspIyGlnIyIleValAspCyIleValArg 60
  |||||||
DB 121 GCCACAGAGATCGCGCCGACAGACGATACAGGCGCATCTGCACTGCTGCGC 180
QY 161 LeuValIyIleIleTrhIySerAspGlyIleArgGlyLeuTyIyGlnIyPheSerValSer 180
  |||||||
DB 481 CTGGTGAAGATCAACCAAGTCGAGGCGATCCGGGGCTGTACAGGCGCTTCAAGTCTCTC 540
QY 181 ValGlnGlyIleIleIleTyIArgAlaAlaTyIyPheGlyValIyAspTrhAlaIySgIy 200
  |||||||
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Db 541 GTCCAGGCAATCATCTACCGGGGCGCTTGGCTGTACGATACGGCCAAAGGC 600
Qy 201 MetLeuProAspProLysAsnThrHisIleValSerTyrPmetIleAlaGlnThrVal 220
Db 601 ATGCTCCCGACCCCAAGAACACAGCATCGTGTGATGATGATCGGACAGCCGTG 660
Qy 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMet 240
Db 661 ACGGCGGTGGCCGCGTGTCTTACCCCTTCAGACAGCGTGGCGCCCATGATGATG 720
Qy 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrrPargLys 260
Db 721 CAGTCCGGGCGCAAGAGAGCTGACATCATGATACAGGGCCCGCTCGACTGTGAAGAG 780
Qy 261 IlePheArgAspGluGlyLysAlaPhePheLysGlyValArgTrrSerAsnValLeuArg 280
Db 781 ATCTTCAGAGATGAGGGGGGCGCAAGGCTTCTTCAAGGTCGCGTGCACAGCTCTCGG 840
Qy 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysValIle 298
Db 841 GGCATGGGGGCGCCCTTCGTGCTGTCTGTACGACGAGCTCAAGAGTGTATC 894

RESULT 3
US-09-185-904A-3
; Sequence 3, Application US/09185904A
; Patent No. US20020177185A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Cleveland, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Willet, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
; TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 660088.420
; CURRENT APPLICATION NUMBER: US/09/185,904A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 897
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-185-904A-3

Alignment Scores:
Pred. No.: 2,32e-200 Length: 897
Score: 1543.00 Matches: 298
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-811-094-33 (1-298) x US-09-185-904A-3 (1-897)
Qy 1 MetThrGlnGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyIleAlaAla 20
Db 1 ATACAGCAACAGGCAATCTCTTCCGCAAGAGCTTCTTGGCCGAGGACATCGCGCGCC 60
Qy 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
Db 61 ATCTCCAGAGCGCCGCGTGTCCGATCGAGCGGTCAGCTGCTCGCGAGGTCCAGAC 120
Qy 41 AlSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
Db 121 GCCAGCAAGCAGATCGCCCGCCGACAGCACTACAGAGGCAATCGGACTCATGTCCGC 180
Qy 61 IleProLysGlnGlnGlyValLeuSerPheTrrPargLysLeuAlaAsnValIleArg 80
```

```
Db 181 ATCCCCAAGAGAGAGGCGCTGTCTCTTCTGGAGGGGCAACCTTGCACATCTTCGC 240
Qy 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
Db 241 TACTTCCCACTCAAGGCCCTCAACTTGGCTTCAGAGATAGTAAAGCAAGCATCTTCTG 300
Qy 101 GlyGlyValAlaAspLysHisThrGlnPheTrrPargTyrPheAlaGlnLeuAlaSerGly 120
Db 301 GGGGGCGGTGACAAAGCAGACAGCATGTTCTGAGGACTTTCGCGGCAACCTCGCCCGCC 360
Qy 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgTrrArg 140
Db 361 GGTGGCGCCGCGGAGCTTCTCTCTGTGTGTGATCCCGGTGGATTTTGGCAGAACCCGC 420
Qy 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGlnPheArgGlyLeuGlyAspCys 160
Db 421 CTGGACAGGAGACGTTGGGAAAGTACGACAGAGGCGCAGTTCCAGGCGCTGGAGACTTC 480
Qy 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
Db 481 CTGTGAAAGATCACCAAGTCCGACGCGCATCCGGGGCGCTGTACACAGGCGCTTCAGTCTCC 540
Qy 181 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
Db 541 GTCCAGGCAATCATCTACCGGGGCGCTTGGCTGTACGATACGGCCAAAGGC 600
Qy 201 MetLeuProAspProLysAsnThrHisIleValValSerTrrPmetIleAlaGlnThrVal 220
Db 601 ATGCTCCCGACCCCAAGAACACAGCATCGTGTGATGATGATGATCGGACAGCCGTG 660
Qy 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMet 240
Db 661 ACGGCGGTGGCCGCGTGTCTTCTTACCCCTTCAGACAGCGTGGCGCCCATGATGATG 720
Qy 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrrPargLys 260
Db 721 CAGTCCGGGCGCAAGAGAGCTGACATCATGATACAGGGCCCGCTGCTGTGAAGAG 780
Qy 261 IlePheArgAspGluGlyLysAlaPhePheLysGlyValArgTrrSerAsnValLeuArg 280
Db 781 ATCTTCAGAGATGAGGGGGGCGCAAGGCTTCTTCAAGGTCGCGTGCACAGCTCTCGG 840
Qy 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysValIle 298
Db 841 GGCATGGGGGCGCCCTTCGTGCTGTCTGTACGACGAGCTCAAGAGTGTATC 894

RESULT 4
US-10-037-270-687
; Sequence 687, Application US/10037270
; Publication No. US20030104529A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yungang
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhilwei
; APPLICANT: Tillinghast, John
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: NO. US20030104529A1el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CJP2B
; CURRENT APPLICATION NUMBER: US/10/037,270
; CURRENT FILING DATE: 2002-01-04
```

PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1104
SOFTWARE: PL-FL-genes Version 1.0
SEQ ID NO: 687
LENGTH: 1212
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (131)..(1027)
US-10-037-270-687

Alignment Scores:
Pred. No.: 3,686-200 Length: 1212
Score: 1543.00 Matches: 298
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-811-094-33 (1-298) x US-10-037-270-687 (1-1212)

QY 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAlaAla 20
DB 131 ATGACGGAACAGCCATCTCTTGGCCAAAGACTTGTGGCGGAGCATGCGCGCGC 190
QY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
DB 191 ATCTCCAAAGCGCGCTGCTCCATCGACGGGCTCAACCTGCTGCTGAGTCCAGCCAG 250
QY 41 AlaserLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
DB 251 GCCAGCAACAGATCGCGCCGACACAGCATCAAGGCTGCTGACATGCTGCTGCTG 310
QY 61 IleProLysGluGlnGlyValIleuSerPheTyrArgGlyAsnLeuAlaAsnValIleArg 80
DB 311 ATCCCAAGAGCAAGCGGCTGCTGCTGCTGAGGGGCAACCTTCCCAAGCTATTCGC 370
QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
DB 371 TACTTCCCACTCAAGCCCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 430
QY 101 GlyGlyValAlaAspLysHisThrGlnPheTyrArgTyrPheAlaGlyAsnLeuAlaSerGly 120
DB 431 GGGGCGCTGACACAGCAGCATGCTGAGGAGTCTTGGGCGCACTGCTGCTGCTGCTG 490
QY 121 GlyAlaAlaGlyAlaThrSerLeuGlyPheValTyrProLeuAspPheAlaArgThrArg 140
DB 491 GGTGCGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 550
QY 141 LeuAlaAlaAspValGlyLysSerGlyTyrGluArgGluPheArgGlyLeuGlyAspCys 160
DB 551 CTGCGACCGGAGCTGGGAAAGTCAGGCAAGGCGAGGCGAGTCCGAGGCTGGGAGACTGC 610
QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
DB 611 CTGCTGAAGATCACCAAGTCGACGCGCATTCGGGGCTGTACAGGCGCTCCAGTGTCTCC 670
QY 181 ValGlnGlyIleIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
DB 671 GTGCAGGGCATCATCTACCTACCGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 730
QY 201 MetLeuProAspProLysAsnThrHisIleValValSerTyrMetIleAlaGlnThrVal 220
DB 731 ATGCTCCCGCAACCCCAAGAACGACATCGTGTGAGTGTGATCCGAGACCTGTG 790
QY 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgTyrArgTyrMetMet 240
DB 791 ACGGCGCTGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 850

QY 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTyrPargLys 260
DB 851 CATTCGGCGCGCAAGAGCATGATCATGTACAGGCGACCGCTGACTGTGGAGGAG 910
QY 261 IlePheArgAspGluGlyGlyAlaPhePheLysGlyAlaTyrPheAsnValLeuArg 280
DB 911 ATCTCAGAGATGAGGGGCGAGGCGCTTCTTCAAGGCTGCTGCTGCTGCTGCTGCTG 970
QY 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysValIle 298
DB 971 GGCATGGGGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1024

RESULT 5

US-10-044-090-152
Sequence 152, Application US/10044090
Publication No. US20020137081A1
GENERAL INFORMATION:
APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
SEQ ID NO: 152
LENGTH: 2592
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No. US20020137081A1 1330214.11
LOCATION: 1131..1929
OTHER INFORMATION: a, t, c, g, or other
US-10-044-090-152

Alignment Scores:
Pred. No.: 3,736-195 Length: 2592
Score: 1510.00 Matches: 296
Percent Similarity: 99.33% Conservative: 2
Best Local Similarity: 98.67% Mismatches: 0
Query Match: 97.86% Indels: 2
DB: 13 Gaps: 0

US-09-811-094-33 (1-298) x US-10-044-090-152 (1-2592)

QY 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAlaAla 20
DB 207 ATGACGGAACAGCCATCTCTTGGCCAAAGACTTGTGGCGGAGCATGCGCGCGC 266
QY 20 allelesThrAlaValAlaProIleGluArg-ValLysLeuLeuGlnValGlnHis 40
DB 267 CATCTCCAAAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 326
QY 40 lAlaserLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
DB 327 AGCCAGCAACAGATCGCGCCGACACAGCATCAAGGCTGCTGCTGCTGCTGCTGCTG 386
QY 60 rGleProLysGluGlnGlyValIleuSerPheTyrArgGlyAsnLeuAlaAsnValIleArg 80
DB 387 GCATCCCAAGAGCAAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 446
QY 80 rGlyThrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
DB 447 GCTACTTCCCACTCAAGCCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 506
QY 100 euGlyGlyAlaAspLysHisThrGlnPheTyrArgTyrPheAlaGlyAsnLeuAlaSerG 120
DB 507 TGGGGGCGCTGAGCAAGCAGCATGCTGAGGAGTCTTGGGAGTCTTGGGAGTCTTGGG 566
QY 120 lGlyAlaAlaGlyAlaThrSerLeuGlyPheValTyrProLeuAspPheAlaArgThr 140
DB 567 GCGTGGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 626

QY 160 rgleuAlAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspC 160
DB 627 GCCTGACAGGAGCTGGGAAAGTCAGACAGACGGAGTCCGAGGCTTGGAGACT 686
QY 160 yslleuValLysIleThrLysSerAspGlyIleArgGlyLeuThrGlnGlyPheSerValS 180
DB 687 GCCTGGTAAAGTACCAAGTCCGAGGATCCGGGGCTGTACAGAGGCTTCAATGTCT 746
QY 180 erValGlnGlyIleIleThrLysArgAlaAlaTyrPheGlyValTyrAspThrAlaLysG 200
DB 747 CCGTCAGAGGATCATCTATCTACCGGGGGCTTACTTGGGCTGTACGATACGGCCAAAG 806
QY 200 lmetleuProAspProLysAsnThrHisIleValIleValSerTrpMetIleAlaGlnThrV 220
DB 807 GCATGCTCCCGACCCCAAGAACAGCACATCGTGTGGTGGATGATTCGGCAGACCG 866
QY 220 alThrAlaValAlaGlyValIleValSerTyrProPheAspThrValArgAlaGlyMetIleM 240
DB 867 TGACGGCCGTGGCGGGCTGTGTCTTACCCCTTGGACAGGGTGGCGGGCCATGATGA 926
QY 240 etGlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgL 260
DB 927 TGACATCGGGGGCGCAAGAGCTGACATCATGTACACGGGCACTTCATCTTGGAGGA 986
QY 260 ysllePheArgAspGluGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuA 280
DB 987 AGATCTCAGAGATGAGGGGGCGCAAGGCTTCTCAAGGGTGGTCCAGGTCCTGC 1046
QY 280 rglMetGlyGlyAlaPheValIleuValIleuTyrAspGluLeuLysValIle 298
DB 1047 GGGGATGGGGGGCGCTTCTGTGTGTCTGTACGAGACTCAAGAGGTGATC 1102

RESULT 6
US-09-811-094-2
Sequence 2, Application US/09811094
Patent No. US2001004414A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clewenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Miller, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Pel, Yezhong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLATOR (ANT),
FILE REFERENCE: 660088.420D4
CURRENT APPLICATION NUMBER: US/09/811,094
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 897
TYPE: DNA
ORGANISM: Homo sapien
US-09-811-094-2

Alignment Scores:
Pred. No.: 3,21e-188 Length: 897
Score: 1454.00 Matches: 274
Percent Similarity: 96.96% Conservative: 13
Best Local Similarity: 92.57% Mismatches: 9
Query Match: 94.23% Indels: 0
Gaps: 0
DB: 9

US-09-811-094-33 (1-298) x US-09-811-094-2 (1-897)

QY 1 MetThrGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyIleAlaAla 20
DB 1 ATGACAGATGCCGATGTCTTCCGCCAAGACTCTTGGCAGGTGGAGTGGCGCGAGCC 60

QY 21 lIeSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
DB 61 ATCTCCAGAGAGCGGCTGAGGCCCATTCAGAGCGGTCACAGCTCTCTGACAGTGCACAT 120
QY 41 AlaserLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
DB 121 GCCACAGCAGATCATCTGACATTAAGCAATACAAAGGATTAAGACTGCTGTCCGT 180
QY 61 lIeProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaSerValIleArg 80
DB 181 ATTCACAGAGACAGAGAACTTGTCTTGTGGCGGTGTAACCTGGCAATGTCAATCA 240
QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
DB 241 TACTTCCCAACCCAGGCTTAACTTCCGCTTCAAGATTAATACAGACAGATCTTCCG 300
QY 101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaserGly 120
DB 301 GGTGTGTGGACAAAGAACCCAGTTTGGCCCTTACTTGGCAGAGGATCTGGCATCGGT 360
QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
DB 361 GGTGCCGAGGGGCCACATCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
DB 421 CTACAGAGCTGATGGGTAAAGCTGAGCTGAAGGATTCGAGGCTCGGTGATCTGC 480
QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
DB 481 CTGGTTAAGATCTACAAATCTATGGATTAAAGGGCTGTACCAAGGCTTTAAAGTCT 540
QY 181 ValGlnGlyIleIleThrLysArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
DB 541 GTGACAGGATTAATCATCTACAGAGCGGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
QY 201 MetLeuProAspProLysAsnThrHisIleValIleValSerTrpMetIleAlaGlnThrVal 220
DB 601 ATGCTTCCGAGTCCCAAGAACACTGCATCATCGATGATGATGATGATGATGATGATGATG 660
QY 221 ThrAlaValAlaGlyValIleSerTyrProPheAspThrValArgArgMetMet 240
DB 661 ACTGTGTGGCCGGGTGACTTCTTATCCATTTGACCCGTCGCCGCGCATGATGATG 720
QY 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260
DB 721 CAGTCAGGCGCAAGAGAACTGCATCATGTACACAGGCAAGCTTACTGTGGCGGAG 780
QY 261 lIePheArgAspGluGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuArg 280
DB 781 ATTGCTCGTGAAGAAGAGGCAAGCTTTTCAAGGGTGAAGTCCCAATGTCTTCACA 840
QY 281 GlyMetGlyGlyAlaPheValIleuValIleuTyrAspGluLeuLysLys 296
DB 841 GGCATGGGTGTGCTTGT 888

RESULT 7
US-09-810-644-2
Sequence 2, Application US/09810644
Patent No. US2002001292A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clewenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Miller, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Pel, Yezhong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLATOR (ANT),
FILE REFERENCE: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR

FILE REFERENCE: 660088.420D3
CURRENT APPLICATION NUMBER: US/09/810.644
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 897
TYPE: DNA
ORGANISM: Homo sapien
US-09-810-644-2

Alignment Scores:
Pred No.: 3 21e-188 Length: 897
Score: 1454.00 Matches: 274
Percent Similarity: 96.96% Conservative: 13
Best Local Similarity: 92.57% Mismatches: 9
Query Match: 94.23% Indels: 0
Gaps: 0

US-09-811-094-33 (1-298) x US-09-810-644-2 (1-897)

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QY 1 MethrtrgluglnAlaIleSerPheAlaLysAphLeuAlaGlyIleAlaAla 20
DB 1 ATGACAGATGCGCATGCTTCTGCGCAAGACTTCTGCGAGGTGAGTGGAGCCGACGC 60
QY 21 IleSerLysThrAlaValAlaAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
DB 61 ATCTCCAGAGCGGGGTAGCGCCCATCGAGCGGTGCAAGCTGCTGCTGAGTGCAGCAT 120
QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnIryLysGlyIleValAspCysIleValArg 60
DB 121 GCCACAGACGATCACTGCGATTAAGCAATCAAGCATTAAGCTCGGTCGCT 180
QY 61 IleProLysGluGlnGlyValLysSerPheTrpArgLysAsnLeuAlaValIleArg 80
DB 181 ATTCCCAAGAGACGAAAGTTCTGCTCTTGGCGCGGTAACTGCGCAATGTCATCAGA 240
QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
DB 241 TACTTCCGACCGAGGCTTAACCTTGCCTCAAGATTAATACAGAGATCTTCG 300
QY 101 GlyGlyValAspLysHisThrGlnPheTrpArgLysPheAlaGlyIleAlaSerGly 120
DB 301 GGTGGTGTGACAGACAGAACCCAGTTTGGCGCTACTTGGCGGAATCGGCATCGGT 360
QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
DB 361 GGTGCGGAGGGGCGACATCCCTGTGTTGTGTACCTTGATTTGGCCGACCGG 420
QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgLysPheArgGlyLeuGlyAspCys 160
DB 421 CTGACGCTGATGTGGTAAAGCTGAGCTGAAAGGAATTCGAGGCTCGGTGATGCG 480
QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
DB 481 CTGCTTAATCTTACAAATGTGATGGATTAAGGCTGTACCAAGGCTTTAACGTCT 540
QY 181 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
DB 541 GTGAGGAGTATATCATCTACCGAGCGCCTACTTGGTGATATGATGACACGCAAGGGA 600
QY 201 MetLeuProAspProLysAsnThrHisIleValIleSerTrpMetIleAlaGlnThrVal 220
DB 601 ATGCTTCCGATCCCAAGACACTCATCATCATCATCATCATCATCATCATCATCAT 660
QY 221 ThrAlaValAlaGlyValAlaSerTyrProPheAspThrValArgArgMetMetMet 240
DB 661 ACTGCTGTTCCCGGTGTGACTTCCATCATCATCATCATCATCATCATCATCATCAT 720
QY 241 GlnSerGlyArgGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260
DB 721 CAGTCAGGGGCGCAAGACATCATCATCATCATCATCATCATCATCATCATCATCAT 780
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QY 261 IlePheArgAspGluGlyIleLysAlaPhePheLysGlyAlaTrpSerAsnValLeuArg 280
DB 781 ATTCGCTCGGATGAGAGGCAAGGCTTTTCAAGGCTGATGATGATGATGATGATGAT 840
QY 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLys 296
DB 841 GCGATGCGTGTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 888
```

RESULT 8
US-09-185-904A-2
Sequence 2, Application US/09185904A

GENERAL INFORMATION:
Patent No. US20020177185A1

APPLICANT: Anderson, Christen M.

APPLICANT: Davis, Robert E.

APPLICANT: Clevenger, William

APPLICANT: Wiley, Sandra Eileen

APPLICANT: Waller, Scott W.

APPLICANT: Szabo, Tomas R.

APPLICANT: Ghosh, Soumitra S.

TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE

TITLE OF INVENTION: TRANSLATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS

TITLE OF INVENTION: THEREFOR

FILE REFERENCE: 660088.420

CURRENT APPLICATION NUMBER: US/09/185.904A

CURRENT FILING DATE: 1998-11-03

NUMBER OF SEQ ID NOS: 33

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 2

LENGTH: 897

TYPE: DNA

ORGANISM: Homo sapien

US-09-185-904A-2

Alignment Scores:

Pred. No.: 3 21e-188 Length: 897
Score: 1454.00 Matches: 274
Percent Similarity: 96.96% Conservative: 13
Best Local Similarity: 92.57% Mismatches: 9
Query Match: 94.23% Indels: 0
Gaps: 0

US-09-811-094-33 (1-298) x US-09-185-904A-2 (1-897)

```
QY 1 MethrtrgluglnAlaIleSerPheAlaLysAphLeuAlaGlyIleAlaAla 20
DB 1 ATGACAGATGCGCATGCTTCTGCGCAAGACTTCTGCGAGGTGAGTGGAGCCGACGC 60
QY 21 IleSerLysThrAlaValAlaAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
DB 61 ATCTCCAGAGCGGGGTAGCGCCCATCGAGCGGTGCAAGCTGCTGCTGAGTGCAGCAT 120
QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnIryLysGlyIleValAspCysIleValArg 60
DB 121 GCCACAGACGATCACTGCGATTAAGCAATCAAGCATTAAGCTCGGTCGCT 180
QY 61 IleProLysGluGlnGlyValLysSerPheTrpArgLysAsnLeuAlaValIleArg 80
DB 181 ATTCCCAAGAGACGAAAGTTCTGCTCTTGGCGCGGTAACTGCGCAATGTCATCAGA 240
QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
DB 241 TACTTCCGACCGAGGCTTAACCTTGCCTCAAGATTAATACAGAGATCTTCG 300
QY 101 GlyGlyValAspLysHisThrGlnPheTrpArgLysPheAlaGlyIleAlaSerGly 120
DB 301 GGTGGTGTGACAGACAGAACCCAGTTTGGCGCTACTTGGCGGAATCGGCATCGGT 360
QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
DB 361 GGTGCGGAGGGGCGACATCCCTGTGTTGTGTACCTTGATTTGGCCGACCGGCT 420
QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgLysPheArgGlyLeuGlyAspCys 160
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Db      421 CTAGACGCTGATGTGGTAAAGCTGAGCTGAAGGAAATTCGAGGCTCGTCACTGC 480
Qy      161 LeuValIleThrLysSerAspGlyIleArgGlyLeuTyrglnGlyPheSerValSer 180
Db      481 CTGCTTAAGATCTACAATCTGATGGGATTAAGGGCCCTTACCAGGCTTTAACGCTCT 540
Qy      181 ValGlnGlyIleIleIleTyrrArgAlaAlaTyrrPheGlyValTyrrAspThrAlaIysGly 200
Db      541 GTGCAGGGTATATATCATCTACCGAGCCGCCCTTCTCGTATCTATGACACTGCAAAAGGA 600
Qy      201 MetLeuProAspProLysAsnThrHisIleValIleSerTrpMetIleAlaGlnThrVal 220
Db      601 ATGCTTCGGATCCCAAGAACCTCATCTGATCAGTGAATGATGTCACAGACTGTC 660
Qy      221 ThrAlaValAlaGlyValValSerTyrrProPheAspThrValArgArgMetMet 240
Db      661 ACTGCTGTTGCCGGGTGACTCTCATTCATTTGACACCGTTGCCGCCGATGATGAG 720
Qy      241 GlnSerGlyArgGlyGlyAlaAspIleMetTyrrThrGlyThrValAspCysTrpArgLys 260
Db      721 CAGTCAAGGCGCAAGAACTGACATCATGTACACAGCAGCAGCTTGACTGCGCGAAG 780
Qy      261 IlePheArgAspGlnGlyGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuArg 280
Db      781 ATTGCTCGATGAAGAGGAGCAAGCTTTTCAAGGGGTGATGCTCAATGTTCTCAGA 840
Qy      281 GlyMetGlyGlyAlaPheValIleuValLeuTyrrAspGlnLeuLysLys 296
Db      841 GGCATGGGTGTGCTTTGTGCTTGTCTGTATGATGAATCAAGAG 888

RESULT 9
US-09-917-800A-1327
; Sequence 1327, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917,800A
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1327
; LENGTH: 1196
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 D12770
US-09-917-800A-1327

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Alignment Scores:
Pred. No.: 6,17e-184 Length: 1196
Score: 1424.00 Matches: 267
Percent Similarity: 95.648 Conservative: 18
Best Local Similarity: 89.608 Mismatches: 13
Query Match: 92.298 Indels: 0
Gaps: 0
US-09-811-094-33 (1-298) x US-09-917-800A-1327 (1-1196)

Qy      1 MetThrGlnGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyIleAlaAla 20
Db      76 ATGGGGATCAGGCTTTGAGCTTCTTAAGAGACTTCTGCGAGTGGCATCGCGCGCC 135
Qy      21 IleSerLysThrAlaValAlaAspProIleGluArgValLysLeuLeuGlnIleHis 40
Db      136 GTCTCCAAACCGCGGTCCGCCGATCGAGAGGTCAAACTGCTGCTGCAAGTCCAGCAT 195
Qy      41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrrLysGlyIleValAspCysIleValArg 60
Db      196 GCACGCAACAGATCATGTGACAGAAACAGTACAAAGCATATGATTGTGTCGAGAGA 255
Qy      61 IleProLysGlnGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80
Db      256 ATCCCCAAAGAGAGGCGCTTCTCTCTCTGAGGGGAAACCTGGCCAAAGTGATCCGG 315
Qy      81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrrLysGlnIlePheLeu 100
Db      316 TACTTCCCAACCCAGACTCTCAACTTCGCCCTTCMAAGACAAAGTCAAGACATCTTCG 375
Qy      101 GlyGlyValAlaAspLysHisThrGlnPheTrpArgTyrrPheAlaGlyAsnLeuAlaSerGly 120
Db      376 GGAGGTGTGATGATCAATGAAGCATGTCTGGCGCTACTTGGCTGAACCTGGCGCTGTGG 435
Qy      121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrrProLeuAspPheAlaArgThrArg 140
Db      436 GGGGAGAGTGGGGCTACCTCCCTCTCTCTGCTTACCACACTGATCTTGACAGCAAG 495
Qy      141 LeuAlaAlaAspValAlaLysSerGlyThrGlnArgGluPheArgGlyLeuGlnLysAspCys 160
Db      496 CTGGCTCCGACCGTGGCCAGAGGATCTTCCACAGGAGTCAATAGGGCTGGGTGACTGG 555
Qy      161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrglnGlyPheSerValSer 180
Db      556 CTCACCAAGATCTTCAAGTCTGATGCTGCGAAGAGGCTCTACCAAGGGTTCAATGCTCTG 615
Qy      181 ValGlnGlyIleIleIleTyrrArgAlaAlaTyrrPheGlyValTyrrAspThrAlaLysGly 200
Db      616 GTGCAGGGCATCTCATCTACAGAGCTGCTACTTGGAGTCTATGACACTGCGCAAGGGG 675
Qy      201 MetLeuProAspProLysAsnThrHisIleValIleSerTrpMetIleAlaGlnThrVal 220
Db      676 ATCTCTCCAGACCCCAAGAAATGTGCACATTTATGTAGCTGGATGATGCCAGATGTG 735
Qy      221 ThrAlaValAlaGlyValValSerTyrrProPheAspThrValArgArgMetMet 240
Db      736 ACAGCGGTGGCGGGGTGGGTGCTCATTCATTTGACACATGCTCGGTGAGATGATGAG 795
Qy      241 GlnSerGlyArgGlyGlyAlaAspIleMetTyrrThrGlyThrValAspCysTrpArgLys 260
Db      796 CAGTCTGGCGCGGAAAGGGCTGATATTATGATACAGCGGCACTTCACTGCTGAGAGAG 855
Qy      261 IlePheArgAspGlnGlyGlyLysAlaPhePheLysGlyValaTrpSerAsnValLeuArg 280
Db      856 ATTCGCAAAAGATGAAGAGCGCAAGCTTTCTTAAAGGTGCTTGTCACAGTACAGAGA 915
Qy      281 GlyMetGlyGlyAlaPheValIleuValLeuTyrrAspGlnLeuLysLysValIle 298
Db      916 GGCATGGGGGTGCTTTGTATGTGATGTATGATGATGATCAAAAAATATGTG 969

RESULT 10
US-10-198-846-13437

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; Sequence 13437, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRL-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; PRIORITY FILING DATE: 2002-07-18
; PRIORITY FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 13437
; LENGTH: 1711
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: 1, 2, 1397, 1398, 1399, 1400, 1401, 1402, 1403, 1404, 1405,
; LOCATION: 1406, 1407, 1408, 1409, 1410, 1411, 1412, 1413, 1414, 1415,
; LOCATION: 1416, 1417, 1418, 1419, 1420, 1421, 1422, 1423, 1424, 1425,
; LOCATION: 1426, 1427, 1428, 1429, 1430, 1431, 1432, 1433, 1434
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: 1335, 1336, 1437, 1438, 1439, 1440, 1441, 1442, 1443, 1444,
; LOCATION: 1445, 1446, 1447, 1448, 1449, 1450, 1451, 1452, 1453, 1454,
; OTHER INFORMATION: n = A,T,C or G
; US-10-198-846-13437

Alignment Scores:
Pred. No.: 1,19e-181 Length: 1711
Score: 1409.00 Matches: 263
Percent Similarity: 94.63% Conservative: 19
Best Local Similarity: 88.26% Mismatches: 16
Query Match: 91.32% Indels: 0
Gaps: 0
DB: 14

US-09-811-094-33 (1-298) x US-10-198-846-13437 (1-1711)
OY 1 MetThGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAla 20
DB 167 ATGGGTGATCAGCGCTGGAGCTTCTTAAGAGCTTCTGCGCGCGCGCTGCC 226
OY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
DB 227 GTCTCCAAACCGCGCTGCGCCCATGAGAGGGTCAAACTGCTGCTGAGTCAAGCAT 286
OY 41 AlaserLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
DB 287 GCCAGCAACAGATCAGTGCAGACACAGCAAGGATCATGATGATGCTGAGCA 346
OY 61 ILPEProLysGluGlnIleValLysSerPheTyrArgLysAsnLeuAlaAsnValIleArg 80
DB 347 ATCCCTAAGAGCAGCGGCTTCTCTCTCTGAGGGGCTAAGCTGGCCAAAGCTGATCCGT 406
OY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
DB 407 TACTTCCCAACCAAGCTCACTCACTTCTGCTCAAGACAGATACAAAGCACTCTCTTA 466
OY 101 GlyAlaValAspLysGlnIleThrGlnPheTyrArgLysAsnLeuAlaSerGly 120
DB 467 GGGGGGTGATGCGCATACAGCACTTCTGCGCTACTTTGCGTGAACCTGGGCTCCGT 526
OY 121 GlyAlaValGlyAlaThrSerLeuGlyPheValTyrProLeuAspPheAlaArgThrArg 140
DB 527 GGGGGCGGTGGGGCCACCTCCCTTGTGCTTGTCTACCGCGCTGAGACTTGTCTAGACCAAG 586

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OY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
DB 587 TTGGCTGCTGATGTGGCGAAGGGCGCGCCGACGATTCATGATGCTGGGCACTGT 646
OY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
DB 647 ATCATCAAGATCTTCAAGCTGATGATGCTGAGGGGCTTACAGGCTTCAAGCTCTC 706
OY 181 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
DB 707 GTCCAAAGCATCATATATATAGAGCTGCTGCTGAGTGTGATGATGATGATGATGATG 766
OY 201 MetLeuProAspProLysAsnThrHisIleValLysSerTyrMetIleAlaGlnThrVal 220
DB 767 ATGCTGCTGACCCCAAGAGCTGATTTTGTGAGCTGATGATGATGATGATGATGATG 826
OY 221 ThrAlaValAlaGlyValLysSerTyrPheAspThrValArgArgArgMetMet 240
DB 827 ACAGCATGCTGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 886
OY 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTyrArgLys 260
DB 887 CAGTCCGCGCGAAGAGGCGCGATATATATGACAGGGGACAGTGTGCTGCTGAGAGAG 946
OY 261 IlePheArgAspGluGlyLysAlaPhePheLysGlyAlaTyrSerAsnValLeuArg 280
DB 947 ATTCGCAAAACAGCAAGAGCAAGCAAGCTTCTTCAAGGCTGCTGCTGCTGCTGCTG 1006
OY 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysValIle 298
DB 1007 GCATGCGCGCTGCTTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1060

RESULT 11
US-09-811-094-1
; Sequence 1, Application US/09811094
; Patent No. US2001004414A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Cleveland, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Willey, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pel, Yashong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLATOR (ANT),
; TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
; FILE REFERENCE: 660088.42004
; CURRENT APPLICATION NUMBER: US/09/811,094
; PRIORITY FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 894
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-811-094-1

Alignment Scores:
Pred. No.: 7.07e-179 Length: 894
Score: 1385.50 Matches: 260
Percent Similarity: 94.30% Conservative: 21
Best Local Similarity: 87.25% Mismatches: 16
Query Match: 89.79% Indels: 1
Gaps: 1
DB: 9

US-09-811-094-33 (1-298) x US-09-811-094-1 (1-894)
OY 1 MetThGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAla 20
DB 1 ATGGGTGATCAGCGCTGGAGCTTCTTAAGAGCTTCTGCGCGCGCTGCC 60

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QY 21 IleserlysthrAlaValAlaProIleGluArgValAllysleuLeuGlnValGlnHis 40
Db 61 GTCTCCAAAGACCGGGTGGCCCCCATCGAGAGGGTCAAACTGGTGTGACAGGTCACAT 120
QY 41 AlaserlysglnlleAlaAlaAspLysGlnTyrLysGlylleValAspCysIleValArg 60
Db 121 GCCAGCAAAACAGATCAGTGTGCTGAGAAAGCATACAAAGGATCTTGTATGTGTGTGAGA 180
QY 61 IleProLysGlnGlnGlnValleuSerPheTyrPargLysIleuValAsnValIleArg 80
Db 181 ATCCCTAAGAGAGAGGGCTTCCTCTCTCTCTGAGGGGTAACCTGGCCAAACGATGACCT 240
QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
Db 241 TACTTCCCAACCCCAACCTCTCAACTTGGCTTCAAGACAAAGATCAAGACGCTCTCTTA 300
QY 101 GlyLysValAspLysHisThrGlnPheTyrPargTyrPheAlaGlnValAsnValIleArg 120
Db 301 GGGGGTGTGGATCGGATTAAGCATGTTCTGGCTTACTTGTGTAACCTGGGCTCCGGT 360
QY 121 GlyAlaAlaGlnValAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
Db 361 GGGGGCGGTGGGGCCACCTCCCTTGGCTTGTCTACCCGCTGACCTTGTCTAGACACAGG 420
QY 141 LeuAlaAlaAspValGlnLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
Db 421 TTGGCTGCTGATGTGGCAGAGCGCC---GCCACAGCGTGAATTCATGCTGGCGGCTGT 477
QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
Db 478 ATCATCAAGATCTTCAAGTCTGATGGCTGAGGGGGCTTACCAAGGTTTCACAGTCTCT 537
QY 181 ValGlnGlylleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
Db 538 GTCCAGGACATCATATATATAGAGCTGGCTACTTGGAGTCTATGATATGCAAGGGG 597
QY 201 MetLeuProAspProLysAsnThrHisIleValIleSerTyrMetIleAlaGlnThrVal 220
Db 598 ATGCTCCCTGATGCCCAAGACGTCACATTTTGTGTGAGTGTGATGATGATGCCAGAGTGT 657
QY 221 ThrAlaValAlaGlnValAlaSerTyrProPheAspThrValArgArgMetMetMet 240
Db 658 ACGGGAGTGGCAGAGGCTGCTGCTCAACCTTTGACACGTGTGCTGTAACAAATGATATG 717
QY 241 GlnSerGlyArgLysGlnAlaAspIleMetTyrThrGlnThrValAspCysTyrPargLys 260
Db 718 CAGTCCGGCGGGAAGGGGCGCATATATATATGACACGGGACAGTGTACTGTCGAGAGA 777
QY 261 IlePheArgAspGlnGlyLysAlaPhePheLysGlnValArgPheSerAsnValLeuArg 280
Db 778 ATTCGCAAAAGACCAAGAGAGCCCTCTCTCAAAAGTCCCTGCTCCAAATGTGCTGAGA 837
QY 281 GlyMetGlyGlyAlaPheValleuValIleTyrAspGlnLeuLysValIle 298
Db 838 GGCATGGGGGCTCTTGTATGTATGTATGATGATGATGATCAAAAATATATGTC 891

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; CURRENT APPLICATION NUMBER: US/09/810,644
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 894
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-810-644-1

Alignment Scores:
Pred. No.: 7,07e-179 Length: 894
Score: 1385.50 Matches: 260
Percent Similarity: 94.30% Conservative: 21
Best Local Similarity: 87.25% Mismatches: 16
Query Match: 89.79% Indels: 1
DB: Gaps: 1

US-09-811-094-33 (1-298) x US-09-810-644-1 (1-894)
QY 1 MetThrGlnGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyIleAlaAla 20
Db 1 ATGGGTATACACGCTTGAGACTTCTTAAGACTTCTGGCGGGGCTGCCGCTGCC 60
QY 21 IleserlysthrAlaValAlaProIleGluArgValAllysleuLeuGlnValGlnHis 40
Db 61 GTCTCCAAAGACCGGGTGGCCCCCATCGAGAGGGTCAAACTGGTGTGACAGGTCACAT 120
QY 41 AlaserlysglnlleAlaAlaAspLysGlnTyrLysGlylleValAspCysIleValArg 60
Db 121 GCCAGCAAAACAGATCAGTGTGCTGAGAAAGCATACAAAGGATCTTGTATGTGTGAGA 180
QY 61 IleProLysGlnGlnGlnValleuSerPheTyrPargLysIleuValAsnValIleArg 80
Db 181 ATCCCTAAGAGAGAGGGCTTCCTCTCTCTGAGGGGTAACCTGGCCAAACGATGACCT 240
QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
Db 241 TACTTCCCAACCCCAACCTCTCAACTTGGCTTCAAGACAAAGATCAAGACGCTCTCTTA 300
QY 101 GlyLysValAspLysHisThrGlnPheTyrPargTyrPheAlaGlnValAsnValIleArg 120
Db 301 GGGGGTGTGGATCGGATTAAGCATGTTCTGGCTTACTTGTGTAACCTGGGCTCCGGT 360
QY 121 GlyAlaAlaGlnValAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
Db 361 GGGGGCTGGGGCCACCTCCCTTGGCTTGTCTACCCGCTGACCTTGTCTAGACACAGG 420
QY 141 LeuAlaAlaAspValGlnLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
Db 421 TTGGCTGCTGATGTGGCAGAGCGCC---GCCACAGCGTGAATTCATGCTGGCGGCTGT 477
QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
Db 478 ATCATCAAGATCTTCAAGTCTGATGGCTGAGGGGGCTTACCAAGGTTTCACAGTCTCT 537
QY 181 ValGlnGlylleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
Db 538 GTCCAGGACATCATATATATAGAGCTGGCTACTTGGAGTCTATGATATGCAAGGGG 597
QY 201 MetLeuProAspProLysAsnThrHisIleValIleSerTyrMetIleAlaGlnThrVal 220
Db 598 ATGCTCCCTGATGCCCAAGACGTCACATTTTGTGAGTGTGATGATGATGCCAAGTGTG 657
QY 221 ThrAlaValAlaGlnValAlaSerTyrProPheAspThrValArgArgMetMetMet 240
Db 658 ACGGGAGTGGCAGAGGCTGCTGCTCAACCTTTGACACGTGTGCTGTAACAAATGATATG 717
QY 241 GlnSerGlyArgLysGlnAlaAspIleMetTyrThrGlnThrValAspCysTyrPargLys 260
Db 718 CAGTCCGGCGGGAAGGGGCGCATATATATATGACACGGGACAGTGTACTGTCGAGAGA 777
QY 261 IlePheArgAspGlnGlyLysAlaPhePheLysGlnValArgPheSerAsnValLeuArg 280

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Db 778 ATTGCAAAAGCAGAGAGCCAGGCTCTTCAAGAGCTGCTGCTGAGCA 837
OY 281 GYMeTgLyglYAlaPheValLeuValLeuTyrAspGluLeuYsLyValIle 298
Db 838 GGCATGGCGGCTGCTTTGTATTGGTGTATGATGATCAAAATATGTC 891

RESULT 13
US-09-185-904A-1
Sequence 1, Application US/09185904A
Patent No. US2002017185A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Cleveland, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Miller, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
TITLE OF INVENTION: TRANSLATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
FILE REFERENCE: 660088.420
CURRENT FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 894
TYPE: DNA
ORGANISM: Homo sapien
US-09-185-904A-1

Alignment Scores:
Pred. No.: 7.07e-179 Length: 894
Score: 1385.50 Matches: 260
Percent Similarity: 94.30% Conservative: 21
Best Local Similarity: 87.25% Mismatches: 16
Query Match: 89.79% Indels: 1
Gaps: 1

US-09-811-094-33 (1-298) x US-09-185-904A-1 (1-894)
OY 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAla 20
Db 1 ATGGGTGATCAGCGCTGGAGCTCTTAAGAGACTTCTGCGGGGCGGCTGCGCTGCC 60
OY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
Db 61 GTCTCCAAAGACCGCGCTGCCCGCCATCGAGAGGCTCAAACTCTCTCAGGTCACAGAT 120
OY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
Db 121 GCCAGCAAAACAGATCAGTGCAGAGAACAGTACAAAGGAGATGATGATGCTGAGCA 180
OY 61 IleProLysGluGlnGlyValIleLeuSerPheTyrArgGlyAsnLeuAlaAsnValIleArg 80
Db 181 ATCCCTTAAGACAGAGGCTTCTCTCTTGTGAGGGGTAACCTGCGCAACGTATGCTGT 240
OY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
Db 241 TACTTCCCAACCCAGCTCTCACTTCGCTGAGGAGCAAGTACAAACAGCACTCTTCTTA 300
OY 101 GYMeTgLyglYAlaPheValLeuValLeuTyrAspGluLeuYsLyValIle 120
Db 301 GGGGGTGTGATCGATCAAGAGTCTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
OY 121 GYAlaAlaGlyAlaThrSerLeuLysPheValTyrProLeuAspPheAlaArgTyrArg 140
Db 361 GGGGCGCTGGGGCCACCTCCCTTGTGCTGTGTACCCGCTGAGCTTGTGAGGCAAGG 420
OY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160

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Db 421 TTGGCTGCTGATGTGGCGAGCGCC---GCCAGCGTGTGATTCATGCTGTCGCGACTGT 477
OY 161 LeuValLysIleLeuThrLysSerAspGlyIleArgGlyLeuYsLyValIlePheSerValSer 180
Db 478 ATCATCAAGATCTTCAAGTCTGATGCTGAGGGGCTTACAGAGGTTTCAAGCTCTCT 537
OY 181 ValGlnGlyIleIleLeuTyrArgAlaIlePheGlyValLysAspPheAlaLysGly 200
Db 538 GTCCAGGATCATTTATCTATAGCTCTGCTGAGTGTATGATCTGATCTGCAAGGCG 597
OY 201 MetLeuProAspProLysAsnThrHisIleValAlaSerPheIleAlaGlnThrVal 220
Db 598 ATGCTGCTGATACCCCAAGAACCTGATTTTGTGAGCTGATGATGATTCGCCAGAGTGTG 657
OY 221 ThrAlaValAlaGlyValAlaValSerTyrProPheAspThrValArgArgMetMet 240
Db 658 ACGGATGCTGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 717
OY 241 GlnSerGlyArgGlyGlyAlaAspIleMetTyrThrGlyThrValAspCysTyrArgLys 260
Db 718 CAGTCCGCGCGGAAAGGCGCCATTTATGATACAGGGGACAGTGTGCTGCTGAGGAG 777
OY 261 IlePheArgAspGluGlyGlyLysAlaPhePheLysGlyAlaTyrSerAsnValLeuArg 280
Db 778 ATTGCAAAAGCAGAGAGCCAGGCTTCTTCAAGGTCGCTGCTGCTGCTGCTGCTGCTG 837
OY 281 GYMeTgLyglYAlaPheValLeuValLeuTyrAspGluLeuYsLyValIle 298
Db 838 GGCATGGCGGCTGCTTTGTATTGGTGTATGATGATCAAAATATGTC 891

RESULT 14
US-09-969-708-213
Sequence 213, Application US/09969708
Patent No. US20020102532A1
GENERAL INFORMATION:
APPLICANT: Augustus, Means
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign
FILE REFERENCE: 689290-70
CURRENT FILING DATE: 2001-10-03
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Pileup Version 3.0
SEQ ID NO 213
LENGTH: 1116
TYPE: DNA
ORGANISM: Homo sapiens
US-09-969-708-213

Alignment Scores:
Pred. No.: 8.96e-175 Length: 1116
Score: 1356.50 Matches: 260
Percent Similarity: 99.24% Conservative: 1
Best Local Similarity: 98.66% Mismatches: 1
Query Match: 87.91% Indels: 1
Gaps: 1

US-09-811-094-33 (1-298) x US-09-969-708-213 (1-1116)
OY 36 LeuGlnValGlnHisAlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleVal 55
Db 1 CTGCAAGTCCAGCAGCGCAGCAAGCAATGCGCGCGAGCAAGCAATGCGCGCGAGCTG 60
OY 56 AspCysIleValAlaGlyIleProLysGluGlnGlyValLeuSerPheTyrArgGlyAsnLeu 75
Db 61 GACTGATTTGCTGATCTCCCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120

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QY 76 AlaAsnValIleArgTyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyr 95
DB 121 GCCAAGTCATTTCGCTACTTCCCAAGCCCTCAACTGCGCTTCAAGGATTAAGTAC 180
QY 96 LysGlnIlePheLeuGlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGly 115
DB 181 AAGCAGATCTTCTGGGGGGCGGTGACACACACGCGG---TTCTGGAGACTTCTTGGGGG 237
QY 116 AsnLeuAlaSerGlyGlyAlaAlaGlyAlaThrSerLeuGlyPheValTyrProLeuAsp 135
DB 238 AACCTGGCTCCGGGGGCTGCGCGCGGCGGACCTCCCTGCTGCTGCTGACACCGCTGGAT 297
QY 136 PheAlaArgThrArgLeuAlaAlaAspValGlyLysSerGlyThrGlnArgLysPheArg 155
DB 298 TTTCGACAGAACCCGCTGGACCGGACGCGGAAATCAAGACAGACAGCGCGAGTTCCCA 357
QY 156 GlyLeuGlyAspCysLeuValLysIleThrLysSerAspGlyIleArgLysLeuTyrGln 175
DB 358 GGCTTGGGAGACTGCTGTTGTAAGATCACCAAGTCCGACGGCTCCGGGGCTGTACCAAG 417
QY 176 GlyPheSerValSerValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyr 195
DB 418 GGCTTCAGTGTCTCCGTGACAGGACATCATCTACCGGGCGGCTTCCGCGGTAC 477
QY 196 AspThrAlaLysGlyMetLeuProAspProLysAsnThrHisIleValLysSerTrpMet 215
DB 478 GATAGCGCCAGAGCGCATGCTCCCGACCCCAAGAACACACATCTGTGTGAGACTTGATG 537
QY 216 IleAlaGlnThrValThrAlaValAlaGlyValIleSerTyrProPheAspThrValArg 235
DB 538 ATCGGCGACAGCCGTGACGGCGCTGGCGCGGTGTCTTACCCCTTCGACAGGGTCCG 597
QY 236 ArgArgMetMetGlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrVal 255
DB 598 CGGCGCATGATGATGACATGCGCGGCGCAAGAGAGCTGATCATGACAGGCGACCGTC 657
QY 256 AspCysTrpArgLysIlePheArgAspGlyGlyLysAlaPhePheLysGlyAlaTrp 275
DB 658 GACTGTGGAGGAAGATCTTCAGAGATGAGGGGGGAGAGCCCTTCACAGGGTGGCTGG 717
QY 276 SerAsnValLeuArgLysMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLys 295
DB 718 TCCAAGTCTCTGGGGGCGATGGGGGGCGCTTCTGTCTGTCTGTACGACGAGCTCAAG 777
QY 296 LysValIle 298
DB 778 AAGGTATC 786

RESULT 15
US-09-880-107-2096
; Sequence 2096, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2096
; LENGTH: 1116
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 J03592

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US-09-880-107-2096
Alignment Scores:
Pred. No.: 8,96e-175
Score: 1356.50
Percent Similarity: 99.24%
Best Local Similarity: 98.86%
Query Match: 87.91%
DB: 10
Gaps: 1

US-09-811-094-33 (1-298) x US-09-880-107-2096 (1-1116)
QY 36 LeuGlnValGlnHisAlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleVal 55
DB 1 CTTCAGAGTCCAGCAGCCAGCAGACAGATCGCGCGACAGACAGATCAAGAGGCGATCGTG 60
QY 56 AspCysIleValArgLysLeuProLysGlyGlnGlyValLeuSerPheTrpArgLysAsnLeu 75
DB 61 GACTGCATTTGTCGCGATCCCAAGAGAGAGGCGGTCTGTCTTCTGGAGGGCGAACCTT 120
QY 76 AlaAsnValIleArgTyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyr 95
DB 121 GCCAAGTCATTTCGCTACTTCCCAAGCCCTCAACTCCGCTTCAAGGATTAAGTAC 180
QY 96 LysGlnIlePheLeuGlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGly 115
DB 181 AAGCAGATCTTCTGGGGGGCGGTGACACACGCGG---TTCTGGAGACTTCTTGGGGG 237
QY 116 AsnLeuAlaSerGlyGlyAlaAlaGlyAlaThrSerLeuGlyPheValTyrProLeuAsp 135
DB 238 AACCTGGCTCCGGGGGCTGCGCGCGGCGGACCTCCCTGCTGCTGCTGACACCGCTGGAT 297
QY 136 PheAlaArgThrArgLeuAlaAlaAspValGlyLysSerGlyThrGlnArgLysPheArg 155
DB 298 TTTCGACAGAACCCGCTGGACCGGACGCGTGGAAATCAAGACAGACAGCGCGAGTTCCGA 357
QY 156 GlyLeuGlyAspCysLeuValLysIleThrLysSerAspGlyIleArgLysLeuTyrGln 175
DB 358 GGCTTGGGAGACTGCTGTTGTAAGATCACCAAGTCCGACGCGCATCCGGGGCTGTACCA 417
QY 176 GlyPheSerValSerValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyr 195
DB 418 GGCTTCAGTGTCTCCGTGACAGGACATCATCTACCGGGCGGCTTCCGCGGTAC 477
QY 196 AspThrAlaLysGlyMetLeuProAspProLysAsnThrHisIleValLysSerTrpMet 215
DB 478 GATAGCGCCAGAGCGCATGCTCCCGACCCCAAGAACACGACATCGGTGAGCTGATG 537
QY 216 IleAlaGlnThrValThrAlaValAlaGlyValIleSerTyrProPheAspThrValArg 235
DB 538 ATCGGCGACAGCCGTGACGGCGCGGTGGCTGTGTACCCCTTCGACAGGGTCCG 597
QY 236 ArgArgMetMetGlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrVal 255
DB 598 CGGCGCATGATGATGACATGCGCGGCGCAAGAGAGCTGATCATGACAGGCGACCGTC 657
QY 256 AspCysTrpArgLysIlePheArgAspGlyGlyLysAlaPhePheLysGlyAlaTrp 275
DB 658 GACTGTGGAGGAAGATCTTCAGAGATGAGGGGGGAGAGCCCTTCACAGGGTGGCTGG 717
QY 276 SerAsnValLeuArgLysMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLys 295
DB 718 TCCAAGTCTCTGGGGGCGATGGGGGGCGCTTCTGTCTGTCTGTACGACGAGCTCAAG 777
QY 296 LysValIle 298
DB 778 AAGGTATC 786

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Job time : 336 secs

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